GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 06:01:49 ; Search time 777.143 Seconds
(without alignments)
1462.883 Million cell updates/sec

Title: US-10-661-094-1_COPY_898_917
Perfect score: 20
Sequence: 1 ttcaggctcatccttcggtg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	20	6	CS061876	CS061876 Sequence
	2	20	100.0	614	1	AY754011	AY754011 Enterococ
	3	20	100.0	1029	6	AR035505	AR035505 Sequence
	4	20	100.0	1029	6	BD181846	BD181846 Polypepti
	5	20	100.0	1032	6	AX085668	AX085668 Sequence
	6	20	100.0	1032	6	AX111560	AX111560 Sequence
	7	20	100.0	1034	6	CQ797595	CQ797595 Sequence
	8	20	100.0	1218	6	AX110322	AX110322 Sequence
	9	20	100.0	1232	6	AX110321	AX110321 Sequence
	10	20	100.0	1237	6	AX110319	AX110319 Sequence
	11	20	100.0	1241	6	AX110316	AX110316 Sequence
	12	20	100.0	1249	6	AX110317	AX110317 Sequence
	13	20	100.0	1263	6	AX110320	AX110320 Sequence
	14	20	100.0	1265	6	AX110323	AX110323 Sequence
	15	20	100.0	1269	6	AX110324	AX110324 Sequence
	16	20	100.0	1272	6	AX110318	AX110318 Sequence
	17	20	100.0	1768	1	EFPVANAG	X56895 E.faecium p
	18	20	100.0	1768	6	CQ797596	CQ797596 Sequence
	19	20	100.0	1768	6	CQ797597	CQ797597 Sequence
	20	20	100.0	1768	6	CS061873	CS061873 Sequence
	21	20	100.0	1768	6	AX110406	AX110406 Sequence
	22	20	100.0	2607	6	AR089411	AR089411 Sequence
	23	20	100.0	2607	6	AR093611	AR093611 Sequence
	24	20	100.0	2667	6	AR035514	AR035514 Sequence
	25	20	100.0	2667	6	BD181855	BD181855 Polypepti
	26	20	100.0	3946	6	AX110408	AX110408 Sequence
	27	20	100.0	7225	6	AR035512	AR035512 Sequence
	28	20	100.0	7225	6	BD181853	BD181853 Polypepti
	29	20	100.0	10851	1	TRNVAN	M97297 Enterococcu
	30	20	100.0	10851	6	AR035513	AR035513 Sequence
	31	20	100.0	10851	6	BD181854	BD181854 Polypepti
	32	20	100.0	10851	6	AX085648	AX085648 Sequence
	33	20	100.0	17510	1	AF516335	AF516335 Enterococ
	34	20	100.0	57889	1	AE017171	AE017171 Staphyloc
	35	18.4	92.0	786	1	OTPDVANA2	X79049 O.turbata P
c	36	18.4	92.0	186605	9	AL606928	AL606928 Mouse DNA
c	37	18	90.0	399	3	DQ117337	DQ117337 Unculture
c	38	18	90.0	801	3	AY327227	AY327227 Unculture
	39	17.4	87.0	48352	13	AY225134	AY225134 Feldmanni
c	40	17.4	87.0	92474	8	AC131384	AC131384 Homo sapi
	41	17.4	87.0	144542	8	AC015819	AC015819 Homo sapi
	42	17.4	87.0	150214	8	AC091489	AC091489 Homo sapi
	43	17.4	87.0	153596	14	AC130453	AC130453 Homo sapi
	44	17.4	87.0	153773	8	HUAC004020	AC004020 Homo sapi
c	45	17.4	87.0	170711	14	AC032020	AC032020 Homo sapi
	46	17.4	87.0	190048	9	AL591126	AL591126 Mouse DNA
	47	17.4	87.0	190123	14	AC141358	AC141358 Bos tauru
c	48	17.4	87.0	203643	14	AC140525	AC140525 Homo sapi
	49	17.4	87.0	210236	14	AC150699	AC150699 Bos tauru
	50	17.4	87.0	223891	14	AC163846	AC163846 Bos tauru
c	51	17	85.0	812	15	AJ717397	AJ717397 Schedonor
c	52	17	85.0	842	15	AJ717396	AJ717396 Schedonor
c	53	17	85.0	1087	15	AJ786400	AJ786400 Schedonor
c	54	17	85.0	1409	15	AY436639	AY436639 Schedonor
c	55	17	85.0	183689	9	AC138719	AC138719 Mus muscu
c	56	16.8	84.0	201	10	BV207778	BV207778 sqmm22453
c	57	16.8	84.0	277	3	AF406375	AF406375 Unculture
c	58	16.8	84.0	304	3	AF406326	AF406326 Unculture
c	59	16.8	84.0	548	6	BD058535	BD058535 Secreted
	60	16.8	84.0	638	6	AX388755	AX388755 Sequence
	61	16.8	84.0	1054	1	BCY15704	Y15704 Bacillus ci
c	62	16.8	84.0	1107	3	UMBSAR11	X52172 Unknown mar
c	63	16.8	84.0	1119	3	AY664069	AY664069 Unculture
c	64	16.8	84.0	1172	3	AY664067	AY664067 Unculture
c	65	16.8	84.0	1180	3	AY664079	AY664079 Unculture
c	66	16.8	84.0	1187	3	AY664092	AY664092 Unculture
c	67	16.8	84.0	1206	3	AY664083	AY664083 Unculture
c	68	16.8	84.0	1397	3	DQ071046	DQ071046 Unculture
c	69	16.8	84.0	1397	3	DQ071146	DQ071146 Unculture
c	70	16.8	84.0	1397	3	DQ071148	DQ071148 Unculture
c	71	16.8	84.0	1433	3	AF382131	AF382131 Unculture
c	72	16.8	84.0	1959	3	DQ009251	DQ009251 Unculture
c	73	16.8	84.0	2311	8	BC002875	BC002875 Homo sapi
c	74	16.8	84.0	3121	8	HSU88154	U88154 Homo sapien
c	75	16.8	84.0	3186	8	AY882602	AY882602 Homo sapi
c	76	16.8	84.0	3211	6	AR077147	AR077147 Sequence
c	77	16.8	84.0	3211	6	AR170436	AR170436 Sequence
c	78	16.8	84.0	3216	8	BC010457	BC010457 Homo sapi
c	79	16.8	84.0	3393	8	AF547989	AF547989 Homo sapi
c	80	16.8	84.0	3456	8	BC069058	BC069058 Homo sapi
c	81	16.8	84.0	3901	6	AR077146	AR077146 Sequence
c	82	16.8	84.0	3901	6	AR170435	AR170435 Sequence
c	83	16.8	84.0	3910	8	HSU88153	U88153 Homo sapien
	84	16.8	84.0	5000	1	ASU13677	U13677 Anabaena sp
c	85	16.8	84.0	11521	1	AE013459	AE013459 Methanosa
c	86	16.8	84.0	23152	9	AL731720	AL731720 Mouse DNA
	87	16.8	84.0	43190	8	AC005777	AC005777 Homo sapi
	88	16.8	84.0	70978	14	AC027788	AC027788 Homo sapi
	89	16.8	84.0	79995	14	AC022231	AC022231 Mus muscu
	90	16.8	84.0	80419	8	AL139826	AL139826 Human DNA
	91	16.8	84.0	86945	14	AC002490	AC002490 Homo sapi

c 92	16.8	84.0	94023	8	AC008720	AC008720 Homo sapi
93	16.8	84.0	104771	9	AL603830	AL603830 Mouse DNA
94	16.8	84.0	110000	1	BA000019_63	Continuation (64 o
95	16.8	84.0	110000	15	AP008216_130	Continuation (131
c 96	16.8	84.0	119227	15	CR378662	CR378662 M.truncat
97	16.8	84.0	144593	15	AC021891	AC021891 Genomic S
c 98	16.8	84.0	148671	14	AC120316	AC120316 Rattus no
c 99	16.8	84.0	153248	8	AC112191	AC112191 Homo sapi
c 100	16.8	84.0	154353	8	AC027820	AC027820 Homo sapi
c 101	16.8	84.0	154405	8	AC004990	AC004990 Homo sapi
102	16.8	84.0	163043	14	AC124654	AC124654 Homo sapi
c 103	16.8	84.0	166134	9	AC127734	AC127734 Rattus no
104	16.8	84.0	169622	14	AC102421	AC102421 Mus muscu
105	16.8	84.0	174846	14	AC141676	AC141676 Apis mell
106	16.8	84.0	191786	8	AC087274	AC087274 Homo sapi
107	16.8	84.0	192590	14	AC118858	AC118858 Rattus no
c 108	16.8	84.0	192805	8	AC146435	AC146435 Pan trogl
c 109	16.8	84.0	192963	14	AC020736	AC020736 Homo sapi
c 110	16.8	84.0	193896	8	AC048387	AC048387 Homo sapi
c 111	16.8	84.0	195494	8	AC091153	AC091153 Homo sapi
c 112	16.8	84.0	197370	14	AC130442	AC130442 Rattus no
c 113	16.8	84.0	201207	14	AC150689	AC150689 Bos tauru
c 114	16.8	84.0	204620	9	AC163342	AC163342 Mus muscu
115	16.8	84.0	212749	14	AC156177	AC156177 Bos tauru
c 116	16.8	84.0	223613	14	AC126216	AC126216 Rattus no
c 117	16.8	84.0	234160	14	AC117890	AC117890 Rattus no
c 118	16.8	84.0	241475	14	AC132756	AC132756 Rattus no
c 119	16.8	84.0	246246	14	AC103121	AC103121 Rattus no
120	16.8	84.0	262124	14	AC095111	AC095111 Rattus no

ALIGNMENTS

```
RESULT 1
CS061876/c
LOCUS       CS061876                  20 bp    DNA     linear   PAT 13-APR-2005
DEFINITION  Sequence 4 from Patent WO2005028679.
ACCESSION   CS061876
VERSION     CS061876.1  GI:62553770
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Dodgson,K.J.
  TITLE     Method and kit for identifying vancomycin-resistant enterococcus
  JOURNAL   Patent: WO 2005028679-A 4 31-MAR-2005;
            University of Iowa Research Foundation (US); DODGSON, Kirsty Jane
            (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db         20 TTCAGGCTCATCCTTCGGTG 1


RESULT 2
AY754011
LOCUS       AY754011                  614 bp    DNA     linear   BCT 19-JAN-2005
DEFINITION  Enterococcus faecium vancomycin resistance protein A (vanA) gene,
            partial cds.
ACCESSION   AY754011
VERSION     AY754011.1  GI:57790303
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1  (bases 1 to 614)
  AUTHORS   Khudaier,B.Y., Shafiani,S., Tewari,R. and Taneja,N.
  TITLE     Detection and molecular characterization of vancomycin resistance
            genes from clinical strains of Enterococci
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 614)
  AUTHORS   Khudaier,B.Y., Shafiani,S., Tewari,R. and Taneja,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-SEP-2004) Biotechnology, Panjab University,
            Sector-14, Chandigarh, U.T 160014, India
FEATURES             Location/Qualifiers
     source          1. .614
                     /organism="Enterococcus faecium"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1352"
     gene            <1. .>614
                     /gene="vanA"
     CDS             <1. .>614
                     /gene="vanA"
                     /codon_start=1
                     /transl_table=11
                     /product="vancomycin resistance protein A"
                     /protein_id="AAW56079.1"
                     /db_xref="GI:57790304"
                     /translation="LVKKNHEYEINHVDVAFSALHGKSGEDGSIQGLFELSGIPFVGC
                     DIQSSAICMDKSLTYIVAKNAGIATPAFWVINKDDRPVAATFTYPVFVKPARSGSSFG
                     VKKVNSADELDYAIESARQYDSKILIEQAVSGCEVGCAVLGNSAALAVGEVDQIRLQY
                     GIFRIHQEVEPEKGSENAVITVPADLSAEERGRIQETAKKIYKAL"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 1;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        288 TTCAGGCTCATCCTTCGGTG 307


RESULT 3
AR035505
LOCUS       AR035505                1029 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5871910.
ACCESSION   AR035505
VERSION     AR035505.1  GI:5952173
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1029)
  AUTHORS   Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
  TITLE     Probes for the detection of nucleotide sequences implicated in the
            expression of resistance to glycopeptides, in particular in
            gram-positive bacteria
  JOURNAL   Patent: US 5871910-A 3 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .1029
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 1029;
  Best Local Similarity   100.0%;  Pred. No. 7.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
```

```
Db        522 TTCAGGCTCATCCTTCGGTG 541


RESULT 4
BD181846
LOCUS       BD181846                1029 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Polypeptides implicated in the expression of resistance to
            glycopeptides, in particular in gram-positive bacteria, nucleotide
            sequence cod ing for these polypeptides and use for diagnosis.
ACCESSION   BD181846
VERSION     BD181846.1  GI:30792764
KEYWORDS    JP 2002320494-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1029)
  AUTHORS   Arthur,M., DuktaMmalen,S., Molinas,C. and Courvalin,P.
  TITLE     Polypeptides implicated in the expression of resistance to
            glycopeptides, in particular in gram-positive bacteria, nucleotide
            sequence cod ing for these polypeptides and use for diagnosis
  JOURNAL   Patent: JP 2002320494-A 2 05-NOV-2002;
            INSTITUT PASTEUR
COMMENT     OS   Bacteria
            PN   JP 2002320494-A/2
            PD   05-NOV-2002
            PF   21-FEB-2002 JP 2002045484
            PR   31-OCT-1990 FR     90/13579
            PI   MICHEL ARTHUR,SYLVIE DUKTA-MALEN,CATHERINE MOLINAS,PATRICE  PI
              COURVALIN
            PC   C12N15/09,C07K14/315,C07K16/12,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12Q1/04,C12Q1/68,G01N33/53,G01N33/566,G01N33/569//C12P21/08,
            PC   (C12Q1/04,C12R1:01),(C12Q1/68,C12R1:01),C12N15/00,C12N5/00 CC
             Polypeptides implicated in the expression of resistance to  CC
                glycopeptides,
            CC   in particular in gram-positive bacteria, nucleotide sequence
            CC            cod ing for
            CC   these polypeptides and use for diagnosis
            FH   Key             Location/Qualifiers
            FT   source          1. .1029
            FT                   /organism='Bacteria'.
FEATURES              Location/Qualifiers
     source           1. .1029
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 1029;
  Best Local Similarity   100.0%;  Pred. No. 7.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        522 TTCAGGCTCATCCTTCGGTG 541


RESULT 5
AX085668
LOCUS       AX085668                1032 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 21 from Patent WO0112803.
ACCESSION   AX085668
VERSION     AX085668.1  GI:13275654
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Inouye,R.T., Torres-Viera,C., Moellering,R., Gold,H. and
            Eliopoulos,G.M.
  TITLE     Methods and compositions for restoring antibiotic susceptibility in
            glycopeptide-resistant Enterococcus
  JOURNAL   Patent: WO 0112803-A 21 22-FEB-2001;
            Beth Israel Deaconess Medical Center, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .1032
                      /organism="Enterococcus faecium"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 1032;
  Best Local Similarity   100.0%;  Pred. No. 7.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        522 TTCAGGCTCATCCTTCGGTG 541


RESULT 6
AX111560
LOCUS       AX111560                1032 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 2293 from Patent WO0123604.
ACCESSION   AX111560
VERSION     AX111560.1  GI:13927852
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 2293 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES              Location/Qualifiers
     source           1. .1032
                      /organism="Enterococcus faecium"
                      /mol_type="unassigned DNA"
                      /strain="BM4147"
                      /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 1032;
  Best Local Similarity   100.0%;  Pred. No. 7.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        522 TTCAGGCTCATCCTTCGGTG 541


RESULT 7
CQ797595
LOCUS       CQ797595                1034 bp    DNA     linear   PAT 20-APR-2004
DEFINITION  Sequence 9 from Patent EP1408120.
ACCESSION   CQ797595
VERSION     CQ797595.1  GI:46425887
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Cockerill,F.R. and Sloan,L.M.
  TITLE     Detection of vancomycin-resistant Enterococcus spp
  JOURNAL   Patent: EP 1408120-A 9 14-APR-2004;
            MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES              Location/Qualifiers
     source           1. .1034
                      /organism="Enterococcus faecium"
                      /mol_type="unassigned DNA"
```

```
                     /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 1034;
  Best Local Similarity   100.0%;  Pred. No. 7.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        522 TTCAGGCTCATCCTTCGGTG 541


RESULT 8
AX110322
LOCUS       AX110322                1218 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1055 from Patent WO0123604.
ACCESSION   AX110322
VERSION     AX110322.1  GI:13926614
KEYWORDS    .
SOURCE      Enterococcus gallinarum
  ORGANISM  Enterococcus gallinarum
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1055 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1218
                     /organism="Enterococcus gallinarum"
                     /mol_type="unassigned DNA"
                     /strain="R684"
                     /db_xref="taxon:1353"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 1218;
  Best Local Similarity   100.0%;  Pred. No. 7.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        596 TTCAGGCTCATCCTTCGGTG 615


RESULT 9
AX110321
LOCUS       AX110321                1232 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1054 from Patent WO0123604.
ACCESSION   AX110321
VERSION     AX110321.1  GI:13926613
KEYWORDS    .
SOURCE      Enterococcus faecalis
  ORGANISM  Enterococcus faecalis
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1054 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1232
                     /organism="Enterococcus faecalis"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1351"
                     /note="R610"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 1232;
  Best Local Similarity   100.0%;  Pred. No. 7.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        606 TTCAGGCTCATCCTTCGGTG 625


RESULT 10
AX110319
LOCUS       AX110319                1237 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1052 from Patent WO0123604.
ACCESSION   AX110319
VERSION     AX110319.1  GI:13926611
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1052 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1237
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /strain="R492"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 1237;
  Best Local Similarity   100.0%;  Pred. No. 7.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        618 TTCAGGCTCATCCTTCGGTG 637


RESULT 11
AX110316
LOCUS       AX110316                1241 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1049 from Patent WO0123604.
ACCESSION   AX110316
VERSION     AX110316.1  GI:13926608
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1049 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1241
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /strain="R690"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 1241;
  Best Local Similarity   100.0%;  Pred. No. 7.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        589 TTCAGGCTCATCCTTCGGTG 608


RESULT 12
AX110317
LOCUS       AX110317               1249 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1050 from Patent WO0123604.
ACCESSION   AX110317
VERSION     AX110317.1  GI:13926609
KEYWORDS    .
SOURCE      Enterococcus gallinarum
  ORGANISM  Enterococcus gallinarum
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1050 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1249
                     /organism="Enterococcus gallinarum"
                     /mol_type="unassigned DNA"
                     /strain="R691"
                     /db_xref="taxon:1353"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 1249;
  Best Local Similarity  100.0%;  Pred. No. 7.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        618 TTCAGGCTCATCCTTCGGTG 637


RESULT 13
AX110320
LOCUS       AX110320               1263 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1053 from Patent WO0123604.
ACCESSION   AX110320
VERSION     AX110320.1  GI:13926612
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1053 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1263
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /strain="R581"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 1263;
  Best Local Similarity  100.0%;  Pred. No. 7.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        610 TTCAGGCTCATCCTTCGGTG 629


RESULT 14
AX110323
LOCUS       AX110323               1265 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1056 from Patent WO0123604.
ACCESSION   AX110323
VERSION     AX110323.1  GI:13926615
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1056 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1265
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /strain="R688"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 1265;
  Best Local Similarity  100.0%;  Pred. No. 7.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        620 TTCAGGCTCATCCTTCGGTG 639


RESULT 15
AX110324
LOCUS       AX110324               1269 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1057 from Patent WO0123604.
ACCESSION   AX110324
VERSION     AX110324.1  GI:13926616
KEYWORDS    .
SOURCE      Enterococcus flavescens
  ORGANISM  Enterococcus flavescens
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1057 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1269
                     /organism="Enterococcus flavescens"
                     /mol_type="unassigned DNA"
                     /strain="R689"
                     /db_xref="taxon:37735"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 1269;
  Best Local Similarity  100.0%;  Pred. No. 7.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        618 TTCAGGCTCATCCTTCGGTG 637
```

```
RESULT 16
AX110318
LOCUS       AX110318               1272 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1051 from Patent WO0123604.
ACCESSION   AX110318
VERSION     AX110318.1  GI:13926610
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1051 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1272
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /strain="R481"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 1272;
  Best Local Similarity   100.0%;  Pred. No. 7.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        598 TTCAGGCTCATCCTTCGGTG 617


RESULT 17
EFPVANAG
LOCUS       EFPVANAG               1768 bp    DNA     linear   BCT 17-JUN-1991
DEFINITION  E.faecium plasmid pIP816 vanA gene for VANA ligase.
ACCESSION   X56895
VERSION     X56895.1  GI:43335
KEYWORDS    D-alanyl-D-alanine ligase; VANA glycopeptide resistance protein;
            vancomycin resistance.
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1  (bases 1 to 1768)
  AUTHORS   Dutka-Malen,S., Molinas,C., Arthur,M. and Courvalin,P.
  TITLE     The VANA glycopeptide resistance protein is related to
            D-alanyl-D-alanine ligase cell wall biosynthesis enzymes
  JOURNAL   Mol. Gen. Genet. 224 (3), 364-372 (1990)
   PUBMED   2266943
REFERENCE   2  (bases 1 to 1768)
  AUTHORS   Dutka-Malen,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-FEB-1991) S. Dutka-Malen, Institut Pasteur, Unile des
            Agents Antibacterions, 28 rue du Dr Roux, Paris Cedex 15, France
FEATURES             Location/Qualifiers
     source          1. .1768
                     /organism="Enterococcus faecium"
                     /mol_type="genomic DNA"
                     /strain="BM4147"
                     /db_xref="taxon:1352"
                     /plasmid="pIP816"
     RBS             360. .369
     gene            377. .1408
                     /gene="vanA"
     CDS             377. .1408
                     /gene="vanA"
                     /codon_start=1
                     /evidence=experimental
                     /transl_table=11
                     /product="VANA ligase"
                     /protein_id="CAA40215.1"
                     /db_xref="GI:43336"
                     /db_xref="GOA:P25051"
                     /db_xref="UniProt/Swiss-Prot:P25051"
                     /translation="MNRIKVAILFGGCSEEHDVSVKSAIEIAANINKEKYEPLYIGIT
                     KSGVWKMCEKPCAEWENDNCYSAVLSPDKKMHGLLVKKNHEYEINHVDVAFSALHGKS
                     GEDGSIQGLFELSGIPFVGCDIQSSAICMDKSLTYIVAKNAGIATPAFWVINKDDRPV
                     AATFTYPVFVKPARSGSSFGVKKVNSADELDYAIESARQYDSKILIEQAVSGCEVGCA
                     VLGNSAALVVGEVDQIRLQYGIFRIHQEVEPEKGSENAVITVPADLSAEERGRIQETA
                     KKIYKALGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMAAAGIALPELID
                     RLIVLALKG"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 1;  Length 1768;
  Best Local Similarity   100.0%;  Pred. No. 7.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        898 TTCAGGCTCATCCTTCGGTG 917


RESULT 18
CQ797596
LOCUS       CQ797596               1768 bp    DNA     linear   PAT 20-APR-2004
DEFINITION  Sequence 10 from Patent EP1408120.
ACCESSION   CQ797596
VERSION     CQ797596.1  GI:46425888
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Cockerill,F.R. and Sloan,L.M.
  TITLE     Detection of vancomycin-resistant Enterococcus spp
  JOURNAL   Patent: EP 1408120-A 10 14-APR-2004;
            MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .1768
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1352"
                     /note="vanA sequence"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 1768;
  Best Local Similarity   100.0%;  Pred. No. 7.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        898 TTCAGGCTCATCCTTCGGTG 917


RESULT 19
CQ797597
LOCUS       CQ797597               1768 bp    DNA     linear   PAT 20-APR-2004
DEFINITION  Sequence 11 from Patent EP1408120.
ACCESSION   CQ797597
VERSION     CQ797597.1  GI:46425889
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Cockerill,F.R. and Sloan,L.M.
  TITLE     Detection of vancomycin-resistant Enterococcus spp
  JOURNAL   Patent: EP 1408120-A 11 14-APR-2004;
            MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES             Location/Qualifiers
```

```
     source          1. .1768
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1352"
                     /note="vanA sequence"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 1768;
  Best Local Similarity   100.0%;  Pred. No. 7.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        898 TTCAGGCTCATCCTTCGGTG 917


RESULT 20
CS061873
LOCUS       CS061873               1768 bp    DNA     linear   PAT 13-APR-2005
DEFINITION  Sequence 1 from Patent WO2005028679.
ACCESSION   CS061873
VERSION     CS061873.1  GI:62553767
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Dodgson,K.J.
  TITLE     Method and kit for identifying vancomycin-resistant enterococcus
  JOURNAL   Patent: WO 2005028679-A 1 31-MAR-2005;
            University of Iowa Research Foundation (US); DODGSON, Kirsty Jane
            (US)
FEATURES             Location/Qualifiers
     source          1. .1768
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 1768;
  Best Local Similarity   100.0%;  Pred. No. 7.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        898 TTCAGGCTCATCCTTCGGTG 917


RESULT 21
AX110406
LOCUS       AX110406               1768 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1139 from Patent WO0123604.
ACCESSION   AX110406
VERSION     AX110406.1  GI:13926698
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1139 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1768
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /strain="BM4147"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 1768;
  Best Local Similarity   100.0%;  Pred. No. 7.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db        898 TTCAGGCTCATCCTTCGGTG 917


RESULT 22
AR089411
LOCUS       AR089411               2607 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 170 from patent US 5994066.
ACCESSION   AR089411
VERSION     AR089411.1  GI:10016168
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2607)
  AUTHORS   Bergeron,M.G., Picard,F.J., Ouellette,M. and Roy,P.H.
  TITLE     Species-specific and universal DNA probes and amplification primers
            to rapidly detect and identify common bacterial pathogens and
            associated antibiotic resistance genes from clinical specimens for
            routine diagnosis in microbiology laboratories
  JOURNAL   Patent: US 5994066-A 170 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .2607
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 2607;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db       1483 TTCAGGCTCATCCTTCGGTG 1502


RESULT 23
AR093611
LOCUS       AR093611               2607 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 170 from patent US 6001564.
ACCESSION   AR093611
VERSION     AR093611.1  GI:10020360
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2607)
  AUTHORS   Bergeron,M.G., Ouellette,M. and Roy,P.H.
  TITLE     Species specific and universal DNA probes and amplification primers
            to rapidly detect and identify common bacterial pathogens and
            associated antibiotic resistance genes from clinical specimens for
            routine diagnosis in microbiology laboratories
  JOURNAL   Patent: US 6001564-A 170 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .2607
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 2607;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db       1483 TTCAGGCTCATCCTTCGGTG 1502
```

```
RESULT 24
AR035514
LOCUS       AR035514                2667 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 17 from patent US 5871910.
ACCESSION   AR035514
VERSION     AR035514.1  GI:5952182
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2667)
  AUTHORS   Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
  TITLE     Probes for the detection of nucleotide sequences implicated in the
            expression of resistance to glycopeptides, in particular in
            gram-positive bacteria
  JOURNAL   Patent: US 5871910-A 17 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .2667
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 2667;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db       1546 TTCAGGCTCATCCTTCGGTG 1565


RESULT 25
BD181855
LOCUS       BD181855                2667 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Polypeptides implicated in the expression of resistance to
            glycopeptides, in particular in gram-positive bacteria, nucleotide
            sequence cod ing for these polypeptides and use for diagnosis.
ACCESSION   BD181855
VERSION     BD181855.1  GI:30792773
KEYWORDS    JP 2002320494-A/11.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2667)
  AUTHORS   Arthur,M., DuktaMmalen,S., Molinas,C. and Courvalin,P.
  TITLE     Polypeptides implicated in the expression of resistance to
            glycopeptides, in particular in gram-positive bacteria, nucleotide
            sequence cod ing for these polypeptides and use for diagnosis
  JOURNAL   Patent: JP 2002320494-A 11 05-NOV-2002;
            INSTITUT PASTEUR
COMMENT     OS   Bacteria
            PN   JP 2002320494-A/11
            PD   05-NOV-2002
            PF   21-FEB-2002 JP 2002045484
            PR   31-OCT-1990 FR     90/13579
            PI   MICHEL ARTHUR,SYLVIE DUKTA-MALEN,CATHERINE MOLINAS,PATRICE  PI
              COURVALIN
            PC   C12N15/09,C07K14/315,C07K16/12,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12Q1/04,C12Q1/68,G01N33/53,G01N33/566,G01N33/569//C12P21/08,
            PC   (C12Q1/04,C12R1:01),(C12Q1/68,C12R1:01),C12N15/00,C12N5/00 CC
             Polypeptides implicated in the expression of resistance to  CC
                 glycopeptides,
            CC   in particular in gram-positive bacteria, nucleotide sequence
            CC            cod ing for
            CC   these polypeptides and use for diagnosis
            FH   Key             Location/Qualifiers
            FT   source          1. .2667
            FT                   /organism='Bacteria'.
FEATURES             Location/Qualifiers
     source          1. .2667
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 2667;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db       1546 TTCAGGCTCATCCTTCGGTG 1565


RESULT 26
AX110408
LOCUS       AX110408                3946 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1141 from Patent WO0123604.
ACCESSION   AX110408
VERSION     AX110408.1  GI:13926700
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1141 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .3946
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /strain="BM4147"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 3946;
  Best Local Similarity   100.0%;  Pred. No. 7.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db       1483 TTCAGGCTCATCCTTCGGTG 1502


RESULT 27
AR035512
LOCUS       AR035512                7225 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 15 from patent US 5871910.
ACCESSION   AR035512
VERSION     AR035512.1  GI:5952180
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7225)
  AUTHORS   Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
  TITLE     Probes for the detection of nucleotide sequences implicated in the
            expression of resistance to glycopeptides, in particular in
            gram-positive bacteria
  JOURNAL   Patent: US 5871910-A 15 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .7225
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 7225;
  Best Local Similarity   100.0%;  Pred. No. 8;
```

```
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db       5044 TTCAGGCTCATCCTTCGGTG 5063


RESULT 28
BD181853
LOCUS       BD181853                7225 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Polypeptides implicated in the expression of resistance to
            glycopeptides, in particular in gram-positive bacteria, nucleotide
            sequence cod ing for these polypeptides and use for diagnosis.
ACCESSION   BD181853
VERSION     BD181853.1  GI:30792771
KEYWORDS    JP 2002320494-A/9.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 7225)
  AUTHORS   Arthur,M., DuktaMmalen,S., Molinas,C. and Courvalin,P.
  TITLE     Polypeptides implicated in the expression of resistance to
            glycopeptides, in particular in gram-positive bacteria, nucleotide
            sequence cod ing for these polypeptides and use for diagnosis
  JOURNAL   Patent: JP 2002320494-A 9 05-NOV-2002;
            INSTITUT PASTEUR
COMMENT     OS   Bacteria
            PN   JP 2002320494-A/9
            PD   05-NOV-2002
            PF   21-FEB-2002 JP 2002045484
            PR   31-OCT-1990 FR     90/13579
            PI   MICHEL ARTHUR,SYLVIE DUKTA-MALEN,CATHERINE MOLINAS,PATRICE  PI
              COURVALIN
            PC   C12N15/09,C07K14/315,C07K16/12,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12Q1/04,C12Q1/68,G01N33/53,G01N33/566,G01N33/569//C12P21/08,
            PC   (C12Q1/04,C12R1:01),(C12Q1/68,C12R1:01),C12N15/00,C12N5/00 CC
             Polypeptides implicated in the expression of resistance to  CC
                  glycopeptides,
            CC   in particular in gram-positive bacteria, nucleotide sequence
            CC            cod ing for
            CC   these polypeptides and use for diagnosis
            FH   Key             Location/Qualifiers
            FT   source          1. .7225
            FT                   /organism='Bacteria'.
FEATURES             Location/Qualifiers
     source          1. .7225
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 7225;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db       5044 TTCAGGCTCATCCTTCGGTG 5063


RESULT 29
TRNVAN
LOCUS       TRNVAN                  10851 bp    DNA     linear   BCT 20-JUN-2002
DEFINITION  Enterococcus faecium transposon Tn1546 transposase, resolvase, vanR
            (vanR), vanS (vanS), vanH (vanH), vanA (vanA), vanX (vanX), vanY
            (vanY), and teicoplanin resistance protein (vanZ) genes, complete
            cds.
ACCESSION   M97297
VERSION     M97297.1  GI:155036
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1  (bases 1 to 10851)
  AUTHORS   Arthur,M., Molinas,C., Depardieu,F. and Courvalin,P.
  TITLE     Characterization of Tn1546, a Tn3-related transposon conferring
            glycopeptide resistance by synthesis of depsipeptide peptidoglycan
            precursors in Enterococcus faecium BM4147
  JOURNAL   J. Bacteriol. 175 (1), 117-127 (1993)
  PUBMED    8380148
REFERENCE   2  (bases 1 to 10851)
  AUTHORS   Arthur,M., Depardieu,F., Molinas,C., Reynolds,P. and Courvalin,P.
  TITLE     The vanZ gene of Tn1546 from Enterococcus faecium BM4147 confers
            resistance to teicoplanin
  JOURNAL   Gene 154 (1), 87-92 (1995)
  PUBMED    7867956
FEATURES             Location/Qualifiers
     source          1. .10851
                     /organism="Enterococcus faecium"
                     /mol_type="genomic DNA"
                     /specimen_voucher="BM4147"
                     /db_xref="taxon:1352"
                     /tissue_lib="BM 4147"
     repeat_region   1. .10851
                     /transposon="Tn1546"
     repeat_region   1. .38
                     /rpt_type=inverted
                     /transposon="Tn1546"
     CDS             complement(75. .3041)
                     /codon_start=1
                     /transl_table=11
                     /product="transposase"
                     /protein_id="AAA65951.1"
                     /db_xref="GI:155037"
                     /translation="MKIARGRELLTPEQRQAFMQIPEDEWILGTYFTFSKRDLEIVNK
                     RRREENRLGFAVQLAVLRYPGWPYTHIKSIPDSVIQYISKQIGVSPSSLDHYPQRENT
                     LWDHLKEIRSEYDFVTFTLSEYRMTFKYLHQLALENGDAIHLLHECIDFLRKNKIILP
                     AITTLERMVWEARAMAEKKLFNTVSKSLTNEQKEKLEGIITSQHPSESNKTILGWLKE
                     PPGHPSPETFLKIIERLEYIRGMDLETVQISHLHRNRLLQLSRLGSRYEPYAFRDFQE
                     NKRYSILTIYLLQLTQELTDKAFEIHDRQILSLLSKGRKAQEEIQKQNGKKLNEKVIH
                     FTNIGQALIKAREEKLDVFKVLESVIEWNTFVSSVEEAQELARPADYDYLDLLQKRFY
                     SLRKYTPTLLRVLEFHSTKANEPLLQAVEIIRGMNESGKRKVPDDSPVDFISKRWKRH
                     LYEDDGTTINRHYYEMAVLTELREHVRAGDVSIVGSRQYRDFEEYLFSEDTWNQSKGN
                     TRLSVSLSFEDYITERTSSFNERLKWLAANSNKLDGVSLEKGKLSLARLEKDVPEEAK
                     KFSASLYQMLPRIKLTDLLMDVAHITGFHEQFTHASNNRKPDKEETIIIMAALLGMGM
                     NIGLSKMAEATPGLTYKQLANVSQWRMYEDAMNKAQAILVNFHHKLQLPFYWGDGTTS
                     SSDGMRMQLGVSSLHADANPHYGTGKGATIYRFTSDQFSSYYTKIIHTNSRDAIHVLD
                     GLLHHETDLNIEEHYTDTAGYTDQIFGLTHLLGFKFAPRIRDLSDSKLFTIDKASEYP
                     KLEAILRGQINTKVIKENYEDVLRLAHSIREGTVSASLIMGKLGSYSRQNSLATALRE
                     MGRIEKTIFILNYISDESLRRKIQRGLNKGEAMNGLARAIFFGKQGELRERTIQHQLQ
                     RASALNIIINAISIWNTLHLTTAVEYKKRTGSFNEDLLHHMSPLGWEHINLLGEYHFN
                     SEKVVSLNSLRPLKLS"
     CDS             3187. .3762
                     /codon_start=1
                     /transl_table=11
                     /product="resolvase"
                     /protein_id="AAA65952.1"
                     /db_xref="GI:801883"
                     /translation="MRKIGYIRVSSTNQNPSRQFQQLNEIGMDIIYEEKVSGATKDRE
                     QLQKVLDDLQEDDIIYVTDLTRITRSTQDLFELIDNIRDKKASLKSLKDTWLDLSEDN
                     PYSQFLITVMAGVNQLERDLIRMRQREGIELAKKEGKFKGRLKKYHKNHAGMNYAVKL
                     YKEGNMTVNQICEITNVSRASLYRKLSEVNN"
     gene            3976. .4671
                     /gene="vanR"
     CDS             3976. .4671
                     /gene="vanR"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAA65953.1"
                     /db_xref="GI:155039"
                     /translation="MSDKILIVDDEHEIADLVELYLKNENYTVFKYYTAKEALECIDK
                     SEIDLAILDIMLPGTSGLTICQKIRDKHTYPIIMLTGKDTEVDKITGLTIGADDYITK
                     PFRPLELIARVKAQLRRYKKFSGVKEQNENVIVHSGLVINVNTHECYLNEKQLSLTPT
                     EFSILRILCENKGNVVSSELLFHEIWGDEYFSKSNNTITVHIRHLREKMNDTIDNPKY
```

```
                IKTVWGVGYKIEK"
gene            4649. .5803
                /gene="vanS"
CDS             4649. .5803
                /gene="vanS"
                /codon_start=1
                /transl_table=11
                /protein_id="AAA65954.1"
                /db_xref="GI:801884"
                /translation="MVIKLKNKKNDYSKLERKLYMYIVAIVVVAIVFVLYIRSMIRGK
                LGDWILSILENKYDLNHLDAMKLYQYSIRNNIDIFIYVAIVISILILCRVMLSKFAKY
                FDEINTGIDVLIQNEDKQIELSAEMDVMEQKLNTLKRTLEKREQDAKLAEQRKNDVVM
                YLAHDIKTPLTSIIGYLSLLDEAPDMPVDQKAKYVHITLDKAYRLEQLIDEFFEITRY
                NLQTITLTKTHIDLYYMLVQMTDEFYPQLSAHGKQAVIHAPEDLTVSGDPDKLARVFN
                NILKNAAAYSEDNSIIDITAGLSGDVVSIEFKNTGSIPKDKLAAIFEKFYRLDNARSS
                DTGGAGLGLAIAKEIIVQHGGQIYAESNDNYTTFRVELPAMPDLVDKRRS"
gene            6018. .6986
                /gene="vanH"
CDS             6018. .6986
                /gene="vanH"
                /codon_start=1
                /transl_table=11
                /protein_id="AAA65955.1"
                /db_xref="GI:155041"
                /translation="MNNIGITVVYGCEQDEADAFHALSPRFGVMATIINANVSESNAKS
                APFNQCISVGHKSEISASILLALKRAGVKYISTRSIGCNHIDTTAAKRMGITVDNVAY
                SPDSVADYTMMLILMAVRNVKSIVRSVEKHDFRLDSDRGKVLSDMTVGVVGTGQIGKA
                VIERLRGFGCKVLAYSRSRSIEVNYVPFDELLQNSDIVTLHVPLNTDTHYIISHEQIQ
                RMKQGAFLINTGRGPLVDTYELVKALENGKLGGAALDVLEGEEEFFYSDCTQKPIDNQ
                FLLKLQRMPNVIITPHTAYYTEQALRDTVEKTIKNCLDFERRQEHE"
gene            6979. .8010
                /gene="vanA"
CDS             6979. .8010
                /gene="vanA"
                /codon_start=1
                /transl_table=11
                /protein_id="AAA65956.1"
                /db_xref="GI:155042"
                /translation="MNRIKVAILFGGCSEEHDVSVKSAIEIAANINKEKYEPLYIGIT
                KSGVWKMCEKPCAEWENDNCYSAVLSPDKKMHGLLVKKNHEYEINHVDVAFSALHGKS
                GEDGSIQGLFELSGIPFVGCDIQSSAICMDKSLTYIVAKNAGIATPAFWVINKDDRPV
                AATFTYPVFVKPARSGSSFGVKKVNSADELDYAIESARQYDSKILIEQAVSGCEVGCA
                VLGNSAALVVGEVDQIRLQYGIFRIHQEVEPEKGSENAVITVPADLSAEERGRIQETA
                KKIYKALGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMAAAGIALPELID
                RLIVLALKG"
gene            8016. .8624
                /gene="vanX"
CDS             8016. .8624
                /gene="vanX"
                /codon_start=1
                /transl_table=11
                /protein_id="AAA65957.1"
                /db_xref="GI:155043"
                /translation="MEIGFTFLDEIVHGVRWDAKYATWDNFTGKPVDGYEVNRIVGTY
                ELAESLLKAKELAATQGYGLLLWDGYRPKRAVNCFMQWAAQPENNLTKESYYPNIDRT
                EMISKGYVASKSSHSRGSAIDLTLYRLDTGELVPMGSRFDFMDERSHHAANGISCNEA
                QNRRRLRSIMENSGFEAYSLEWWHYVLRDEPYPNSYFDFPVK"
gene            9052. .9963
                /gene="vanY"
CDS             9052. .9963
                /gene="vanY"
                /codon_start=1
                /transl_table=11
                /protein_id="AAA65958.1"
                /db_xref="GI:155044"
                /translation="MKKLPFLLLLLFLIYLGYDYVNEALFSQEKVEFQNYDQNPKEHL
                ENSGTSENTQEKTITEEQVYQGNLLLINSKYPVRQESVKSDIVNLSKHDELINGYGLL
                DSNIYMSKEIAQKFSEMVNDAVKGGVSHFIINSGYRDFDEQSVLYQEMGAEYALPAGY
                SEHNSGLSLDVGSSLTKMERAPEGKWIEENAWKYGFILRYPEDKTELTGIQYEPWHIR
                YVGLPHSAIMKEKNFVLEEYMDYLKEEKTISVSVNGEKYEIFYYPVTKNTTIHVPTNL
                RYEISGNNIDGVIVTVFPGSTHTNSRR"
gene            10116. .10601
                /gene="vanZ"
CDS             10116. .10601
                /gene="vanZ"
                /codon_start=1
                /transl_table=11
                /product="teicoplanin resistance protein"
                /protein_id="AAA65959.1"
                /db_xref="GI:801885"
                /translation="MGKILSRGLLALYLVTLIWLVLFKLQYNILSVFNYHQRSLNLTP
                FTATGNFREMIDNVIIFIPFGLLLNVNFKEIGFLPKFAFVLVLSLTFEIIQFIPAIGA
                TDITDVITNTVGGFLGLKLYGLSNKHMNQKKLDRVIIFVGILLLVLLLVYRTHLRINY
                V"
repeat_region   10814. .10851
                /rpt_type=inverted
                /transposon="Tn1546"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 1;  Length 10851;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db       7500 TTCAGGCTCATCCTTCGGTG 7519


RESULT 30
AR035513
LOCUS       AR035513               10851 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 16 from patent US 5871910.
ACCESSION   AR035513
VERSION     AR035513.1  GI:5952181
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10851)
  AUTHORS   Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
  TITLE     Probes for the detection of nucleotide sequences implicated in the
            expression of resistance to glycopeptides, in particular in
            gram-positive bacteria
  JOURNAL   Patent: US 5871910-A 16 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .10851
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 10851;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db       7500 TTCAGGCTCATCCTTCGGTG 7519


RESULT 31
BD181854
LOCUS       BD181854               10851 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Polypeptides implicated in the expression of resistance to
            glycopeptides, in particular in gram-positive bacteria, nucleotide
            sequence cod ing for these polypeptides and use for diagnosis.
ACCESSION   BD181854
VERSION     BD181854.1  GI:30792772
KEYWORDS    JP 2002320494-A/10.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10851)
  AUTHORS   Arthur,M., DuktaMmalen,S., Molinas,C. and Courvalin,P.
  TITLE     Polypeptides implicated in the expression of resistance to
            glycopeptides, in particular in gram-positive bacteria, nucleotide
            sequence cod ing for these polypeptides and use for diagnosis
```

```
  JOURNAL   Patent: JP 2002320494-A 10 05-NOV-2002;
            INSTITUT PASTEUR
COMMENT     OS   Bacteria
            PN   JP 2002320494-A/10
            PD   05-NOV-2002
            PF   21-FEB-2002 JP 2002045484
            PR   31-OCT-1990 FR     90/13579
            PI   MICHEL ARTHUR,SYLVIE DUKTA-MALEN,CATHERINE MOLINAS,PATRICE  PI
              COURVALIN
            PC   C12N15/09,C07K14/315,C07K16/12,C12N1/15,C12N1/19,C12N1/21,  PC
             C12N5/10,
            PC   C12Q1/04,C12Q1/68,G01N33/53,G01N33/566,G01N33/569//C12P21/08,
            PC   (C12Q1/04,C12R1:01),(C12Q1/68,C12R1:01),C12N15/00,C12N5/00 CC
             Polypeptides implicated in the expression of resistance to  CC
                glycopeptides,
            CC   in particular in gram-positive bacteria, nucleotide sequence
            CC            cod ing for
            CC   these polypeptides and use for diagnosis
            FH   Key             Location/Qualifiers
            FT   source          1. .10851
            FT                   /organism='Bacteria'.
FEATURES              Location/Qualifiers
     source           1. .10851
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 10851;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db       7500 TTCAGGCTCATCCTTCGGTG 7519


RESULT 32
AX085648
LOCUS       AX085648               10851 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 1 from Patent WO0112803.
ACCESSION   AX085648
VERSION     AX085648.1  GI:13275634
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Inouye,R.T., Torres-Viera,C., Moellering,R., Gold,H. and
            Eliopoulos,G.M.
  TITLE     Methods and compositions for restoring antibiotic susceptibility in
            glycopeptide-resistant Enterococcus
  JOURNAL   Patent: WO 0112803-A 1 22-FEB-2001;
            Beth Israel Deaconess Medical Center, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .10851
                      /organism="Enterococcus faecium"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 10851;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db       7500 TTCAGGCTCATCCTTCGGTG 7519


RESULT 33
AF516335
LOCUS       AF516335               17510 bp    DNA     linear   BCT 28-AUG-2002
DEFINITION  Enterococcus faecium plasmid pUW786 multiple antibiotic resistance
            gene cluster, complete sequence.
ACCESSION   AF516335
VERSION     AF516335.1  GI:21886737
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1  (bases 1 to 17510)
  AUTHORS   Werner,G., Klare,I. and Witte,W.
  TITLE     Multi-resistance gene cluster on a plasmid in a clinical isolate of
            Enterococcus faecium
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 17510)
  AUTHORS   Werner,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAY-2002) Wernigerode Branch, Robert Koch Institute,
            Burgstr. 37, Wernigerode 38855, Germany
FEATURES              Location/Qualifiers
     source           1. .17510
                      /organism="Enterococcus faecium"
                      /mol_type="genomic DNA"
                      /isolate="UW786"
                      /db_xref="taxon:1352"
                      /plasmid="pUW786"
     CDS              <1. .532
                      /codon_start=2
                      /transl_table=11
                      /product="putative resolvase"
                      /protein_id="AAM77881.1"
                      /db_xref="GI:21886738"
                      /translation="PSRQFQQLNEIGMDIIYEEKVSGATKDREQLQKVLDDLQEDDII
                      YVTDLTRITRSTQDLFELIDNIRDKKASLKSLKDTWLDLSEDNPYSQFLITVMAGVNQ
                      LERDLIRMRQREGIELAKKEGKFKGRLKKYHKNHAGMNYAVKLYKEGNMTVNQICEIT
                      NVSRASLYRKLSEVNN"
     repeat_region    <1. .532
                      /transposon="Tn1546"
     gene             746. .1441
                      /gene="vanR"
     CDS              746. .1441
                      /gene="vanR"
                      /note="regulator of two-component regulatory system"
                      /codon_start=1
                      /transl_table=11
                      /product="cytoplasmic regulator"
                      /protein_id="AAM77882.1"
                      /db_xref="GI:21886739"
                      /translation="MSDKILIVDDEHEIADLVELYLKNENYTVFKYYTAKEALECIDK
                      SEIDLAILDIMLPGTSGLTICQKIRDKHTYPIIMLTGKDTEVDKITGLTIGADDYITK
                      PFRPLELIARVKAQLRRYKKFSGVKEQNENVIVHSGLVINVNTHECYLNEKQLSLTPT
                      EFSILRILCENKGNVVSSELLFHEIWGDEYFSKSNNTITVHIRHLREKMNDTIDNPKY
                      IKTVWGVGYKIEK"
     gene             1419. .1463
                      /gene="vanS"
                      /allele="vanS'"
     CDS              1419. .1463
                      /gene="vanS"
                      /allele="vanS'"
                      /codon_start=1
                      /transl_table=11
                      /product="truncated protein kinase"
                      /protein_id="AAM77883.1"
                      /db_xref="GI:21886740"
                      /translation="MVIKLKNKKTTIPN"
     gene             2787. .3755
                      /gene="vanH"
     CDS              2787. .3755
                      /gene="vanH"
                      /codon_start=1
                      /transl_table=11
                      /product="pyruvate dehydrogenase"
```

```
                     /protein_id="AAM77884.1"
                     /db_xref="GI:21886741"
                     /translation="MNNIGITVYGCEQDEADAFHALSPRFGVMATIINANVSESNAKS
                     APFNQCISVGHKSEISASILLALKRAGVKYISTRSIGCNHIDTTAAKRMGITVDNVAY
                     SPDSVADYTMMLILMAVRNVKSIVRSVEKHDFRLDSDRGKVLSDMTVGVVGTGQIGKA
                     VIERLRGFGCKVLAYSRSRSIEVNYVPFDELLQNSDIVTLHVPLNTDTHYIISHEQIQ
                     RMKQGAFLINTGRGPLVDTYELVKALENGKLGGAALDVLEGEEEFFYSDCTQKPIDNQ
                     FLLKLQRMPNVIITPHTAYYTEQALRDTVEKTIKNCLDFERRQEHE"
gene                 3748. .4779
                     /gene="vanA"
CDS                  3748. .4779
                     /gene="vanA"
                     /codon_start=1
                     /transl_table=11
                     /product="D-Ala-D-Lac ligase"
                     /protein_id="AAM77885.1"
                     /db_xref="GI:21886742"
                     /translation="MNRIKVAILFGGCSEEHDVSVKSAIEIAANINKEKYEPLYIGIT
                     KSGVWKMCEKPCAEWENDNCYSAVLSPDKKMHGLLVKKNHEYEINHVDVAFSALHGKS
                     GEDGSIQGLFELSGIPFVGCDIQSSAICMDKSLTYIVAKNAGIATPAFWVINKDDRPV
                     AATFTYPVFVKPARSGSSFGVKKVNSADELDYAIESARQYDSKILIEQAVSGCEVGCA
                     VLGNSAALVVGEVDQIRLQYGIFRIHQEVEPEKGSENAVITVPADLSAEERGRIQETA
                     KKIYKALGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMAAAGIALPELID
                     RLIVLALKG"
gene                 4785. .5393
                     /gene="vanX"
CDS                  4785. .5393
                     /gene="vanX"
                     /codon_start=1
                     /transl_table=11
                     /product="D-Ala-D-Ala dipeptidase"
                     /protein_id="AAM77886.1"
                     /db_xref="GI:21886743"
                     /translation="MEIGFTFLDEIVHGVRWDAKYATWDNFTGKPVDGYEVNRIVGTY
                     ELAESLLKAKELAATQGYGLLLWDGYRPNRAVNCFMQWAAQPENNLTKESYYPNIDRT
                     EMISKGYVASKSSHSRGSAIDLTLYRLDTGELVPMGSRFDFMDERSHHAANGISCNEA
                     QNRRRLRSIMENSGFEAYSLEWWHYVLRDEPYPNSYFDFPVK"
gene                 5821. .6366
                     /gene="vanY"
                     /allele="vanY'"
CDS                  5821. .6366
                     /gene="vanY"
                     /allele="vanY'"
                     /codon_start=1
                     /transl_table=11
                     /product="truncated carboxypeptidase"
                     /protein_id="AAM77887.1"
                     /db_xref="GI:21886744"
                     /translation="MKKLFFLLLLLFLIYLGYDYVNEALFSQEKVEFQNYDQNPKEHL
                     ENSGTSENTQEKTITEEQVYQGNLLLINSKYPVRQESVKSDIVNLSKHDELINGYGLL
                     DSNIYMSKEIAQKFSEMVNDAVKGGVSHFIINSGYRDFDEQSVLYQEMGAEYALPAGY
                     SEHNSGLSLDVGFCCKVLNKE"
repeat_region        complement(6335. .7143)
                     /insertion_seq="IS1216V"
repeat_region        complement(6335. .6352)
                     /note="IR"
                     /rpt_type=inverted
CDS                  complement(6389. .7075)
                     /codon_start=1
                     /transl_table=11
                     /product="transposase"
                     /protein_id="AAM77888.1"
                     /db_xref="GI:21886745"
                     /translation="MTMNHFKGKQFQQDVIIVAVGYYLRYNLSYREVQEILYDRGINV
                     SHTTIYRWVQEYGKLLYQIWKKKNKKSFYSWKMDETYIKIKGKWHYLYRAIDADGLTL
                     DIWLRKKRDTQAAYAFLKRLVKQFDEPKVVVTDKAPSITSAFKKLKEYGFYQGTEHRT
                     IKYLNNLIEQDHRPVKRRNKFYRSLRTASTTIKGMEAIRGLYKKTRKEGTLFGFSVCT
                     EIKVLLGIPA"
repeat_region        complement(7126. .7143)
                     /note="IR"
                     /rpt_type=inverted
CDS                  7537. .7734
                     /codon_start=1
                     /transl_table=11
                     /product="unknown"
                     /protein_id="AAM77889.1"
                     /db_xref="GI:21886746"
                     /translation="MGDKTVRVRADLHHIIKIETAKNGGNVKEVMEIRLRSKLKSVLI
                     VQYLKILCIIGIEVKLDAKNL"
CDS                  7755. .7838
                     /codon_start=1
                     /transl_table=11
                     /product="ermB methylase leader peptide"
                     /protein_id="AAM77890.1"
                     /db_xref="GI:21886747"
                     /translation="MLVFQMRNVDKTSTVLKQTKNSDYTDK"
gene                 7963. .8700
                     /gene="ermB"
CDS                  7963. .8700
                     /gene="ermB"
                     /codon_start=1
                     /transl_table=11
                     /product="ermB methylase"
                     /protein_id="AAM77891.1"
                     /db_xref="GI:21886748"
                     /translation="MNKNIKYSQNFLTSEKVLNQIIKQLNLKETDTVYEIGTGKGHLT
                     TKLAKISKQVTSIELDSHLFNLSSEKLKLNIRVTLIHQDILQFQFPNKQRYKIVGSIP
                     YHLSTQIIKKVVFESHASDIYLIVEEGFYKRTLDIHRTLGLLLHTQVSIQQLLKLPAE
                     CFHPKPKVNSVLIKLTRHTTDVPDKYWKLYTYFVSKWVNREYRQLFTKNQFHQAMKHA
                     KVNNLSTVTYEQVLSIFNSYLLFNGRK"
repeat_region        9136. .>17510
                     /transposon="Tn5405-like"
repeat_region        9136. .9168
                     /note="IS1182 IR-R"
                     /rpt_type=inverted
CDS                  complement(join(9287. .9592,11012. .12001))
                     /note="coding region disrupted by insertion sequence"
                     /codon_start=1
                     /transl_table=11
                     /product="putative transposase"
                     /protein_id="AAM77892.1"
                     /db_xref="GI:21886749"
                     /translation="MNDSIKKMLRITEKDLMITEVSYETLQKKKTLVVDAVLSPTPRA
                     CRSCGSTVVDGNGKAIIVKNGKKETIVRFEQYNHMPLVMRLKKQRYTCKNCRTHWTAQ
                     SYFVQPRHSIANHVRYKIASLLTEKVSLSFIAKSCQVSLTTVIRTLKEFKSYLPKQSK
                     KILPRVLMVDEFRSHASIEDKMSFICADGETGKLIDVLPTRKLPRLTSYFLGCTNPEE
                     VEFLVTDMNAAYFQLTKRVLPNAKVVIDRFHIVKHMNQAFNELRIREMNELRKAGQKS
                     QAEKLKKNWRFLLKNRANINHYEYKTWKSFRAPKYPFLTEAMMIDRLLEFSPPLKEAY
                     PFFHELVEAFRDKDPDLFFSLLAELPETLDDSFREKLQNLLTYEEGITNAMIYPYSNG
                     KIEAKNTHIKTMKRVSYGFKSFENMRIRIFLINQLINVR"
repeat_region        9594. .11009
                     /insertion_seq="IS150-like"
repeat_region        9594. .9613
                     /note="IR-R"
                     /rpt_type=inverted
CDS                  9857. .10183
                     /codon_start=1
```

```
  Query Match             100.0%;  Score 20;  DB 1;  Length 17510;
  Best Local Similarity   100.0%;  Pred. No. 8.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db       4269 TTCAGGCTCATCCTTCGGTG 4288


RESULT 34
AE017171
LOCUS       AE017171               57889 bp    DNA     circular BCT 01-AUG-2003
DEFINITION  Staphylococcus aureus plasmid pLW043, complete sequence.
ACCESSION   AE017171
VERSION     AE017171.1  GI:33390917
KEYWORDS    .
SOURCE      Staphylococcus aureus
  ORGANISM  Staphylococcus aureus
```

```
            Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE   1  (bases 1 to 57889)
  AUTHORS   Gill,S., Kolonay,J., Shetty,J., Tenover,F. and Weigel,L.
  TITLE     Sequence of the Michigan vancomycin-resistant Staphylococcus aureus
            plasmid
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 57889)
  AUTHORS   Gill,S., Kolonay,J., Shetty,J., Tenover,F. and Weigel,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUL-2003) The Institute for Genomic Research, 9712
            Medical Center Dr., Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .57889
                     /organism="Staphylococcus aureus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1280"
                     /plasmid="pLW043"
     gene            101. .1060
                     /gene="repA"
                     /locus_tag="VRA0001"
     CDS             101. .1060
                     /gene="repA"
                     /locus_tag="VRA0001"
                     /note="similar to GP:3676426, and GP:1041637; identified
                     by sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="replication initiator protein"
                     /protein_id="AAQ17124.1"
                     /db_xref="GI:33390918"
                     /translation="MSKQFFTVEENYKERFYQLPKVFFTNPNYKDLSNDAKIAYAILR
                     DRLQLSIKNNWIDTEGNIYFIYTVADLEVILNCGNKKITKIKKELENVDLLIQKRQGL
                     NKPNLLYLLKPAITKNDIYEIDKAENEVEALQDKEVSKGHVQKCQKDTSRNVKRTRLE
                     MSKGHTNDTDFIDTDFIDTESNDMNNMNDTNQHSNHSNHFSNIHDKESLKYIELQELP
                     ELIKSYINNFSYEEVKSIKSVILKAKKSFNNKYDTFYMLEDIDEELLLVLKRFKGYLV
                     KKQEKVANMEGYLMRSIIAELEEMHSTIMRRKNMENNPLSLFN"
     gene            1179. .1853
                     /locus_tag="VRA0002"
     CDS             1179. .1853
                     /locus_tag="VRA0002"
                     /note="similar to GP:13383313, and SP:P19380; identified
                     by sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="IS431mec transposase"
                     /protein_id="AAQ17125.1"
                     /db_xref="GI:33390919"
                     /translation="MNYFRYKQFNKDVITVAVGYYLRYALSYRDISEILRGRGVNVHH
                     STVYRWVQEYAPILYQIWKKKHKKAYYKWRIDETYIKIKGKWSYLYRAIDAEGHTLDI
                     WLRKQRDNHSAYAFIKRLIKQFGKPQKVITDQAPSTKVAMVKVIKAFKLKPDCHCTSK
                     YLNNLIEQDHRHIKVRKTRYQSINTAKNTLKGIECIYALYKKNRRSLQIYGFSPCHEI
                     SIMLAS"
     gene            complement(1885. .2307)
                     /locus_tag="VRA0003"
     CDS             complement(1885. .2307)
                     /locus_tag="VRA0003"
                     /note="similar to GP:4105402; identified by sequence
                     similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="conserved hypothetical protein"
                     /protein_id="AAQ17126.1"
                     /db_xref="GI:33390920"
                     /translation="MAKQIIVTDSTSDLSHEYLKQHNIHVIPLSLTIDGKSYTDQVDI
                     SSSEYIDHIENDADVKTSQPPIGRFIETYEQLAQDDVEIISIHLSSGLSGTYNTAVQA
                     SHMVDGNITVIDSKSISFGLGYQIKQIVELVLLQSKKI"
     gene            complement(2317. .2802)
                     /gene="dfrA"
                     /locus_tag="VRA0004"
     CDS             complement(2317. .2802)
                     /gene="dfrA"
                     /locus_tag="VRA0004"
                     /note="similar to GP:13383309, and SP:P11045; identified
                     by sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="trimethoprim resistant dihydrofolate reductase"
                     /protein_id="AAQ17127.1"
                     /db_xref="GI:33390921"
                     /translation="MTLSIIVAHDKQRVIGYQNQLPWHLPNDLKHIKQLTTGNTLVMA
                     RKTFNSIGKPLPNRRNVVLTNQASFHHEGVDVINSLDEIKELSGHVFIFGGQTLYEAM
                     IDQVDDMYITVIDGKFQGDTFFPPYTFENWEVESSVEGQLDEKNTIPHTFLHLVRRKG
                     K"
     gene            complement(2844. .3800)
                     /gene="thyA"
                     /locus_tag="VRA0005"
     CDS             complement(2844. .3800)
                     /gene="thyA"
                     /locus_tag="VRA0005"
                     /note="similar to SP:P13954, and SP:P00469; identified by
                     sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="thymidylate synthase"
                     /protein_id="AAQ17128.1"
                     /db_xref="GI:33390922"
                     /translation="MYNPFDEAYHGLCEEILEIGNRRDDRTHTGTISKFGHQLRFDLT
                     KGFPLLTTKKVSFKLVATELLWFIKGDTNIQYLLKYNNNIWNEWAFENYVQSDDYHGP
                     DMTDFGHRSQQDPEFNEQYKEEMKKFKERILNDDAFAKKYGNLGNVYGKQWRDWEDKN
                     GNHYDQLKSVIQQIKTNPNSRRHIVSAWNPTEIDSMALPPCHTMFQFYVQEGKLNCQL
                     YQRSADIFLGVPFNIASYALLTHLVAKECGLEVGEFIHTFGDAHIYSNHMDAIHTQLS
                     RDSYLPPQLKINTDKSIFDINYEDLELINYESHPAIKAPIAV"
     gene            3914. .4588
                     /locus_tag="VRA0006"
     CDS             3914. .4588
                     /locus_tag="VRA0006"
                     /note="similar to SP:P14506, and SP:P19380; identified by
                     sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="IS431mec transposase"
                     /protein_id="AAQ17129.1"
                     /db_xref="GI:33390923"
                     /translation="MNYFRYKQFNKDVITVAVGYYLRYALSYRDISEILRGRGVNVHH
                     STVYRWVQEYAPILYQIWKKKHKKAYYKWRIDETYIKIKGKWSYLYRAIDAEGHTLDI
                     WLRKQRDNHSAYAFIKRLIKQFGKPQKVITDQAPSTKVAMAKVIKAFKLKPDCHCTSK
                     YLNNLIEQDHRHIKVRKTRYQSINTAKNTLKGIECIYALYKKNRRSLQIYGFSPCHEI
                     SIMLAS"
     gene            complement(4697. .4885)
                     /gene="artA"
                     /locus_tag="VRA0007"
     CDS             complement(4697. .4885)
                     /gene="artA"
                     /locus_tag="VRA0007"
                     /note="similar to GP:21623785; identified by sequence
                     similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="regulator of transfer gene ArtA"
                     /protein_id="AAQ17130.1"
                     /db_xref="GI:33390924"
                     /translation="MNNNEENSVFFGKKKKVSLHLLVDPDMKDEIIKYAQEKDFDNVS
                     QAGREILKKGLEQIKSNK"
     gene            5057. .6031
                     /gene="traA"
                     /locus_tag="VRA0008"
     CDS             5057. .6031
                     /gene="traA"
                     /locus_tag="VRA0008"
                     /note="similar to GP:3676435, GB:X15505, GB:D45417,
                     SP:P15951, SP:P35030, and PID:37460; identified by
                     sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="TraA"
                     /protein_id="AAQ17131.1"
```

```
                     /db_xref="GI:33390925"
                     /translation="MDNITFRKRIEEYRKRSIEQKKYESKLNYQSRFGVKDDEVSTFN
                     IKGIATDKKENKLVMAEDREDKQKVLLYANKDNDMYYLNSGSTYKEAVQNTFGNETNY
                     EMVDDELFIYNSKNQALTNYDQLDEYHNRQKQLQYNTKLEQERKQRLTDTNKVSENAK
                     EDLALSLGLTATALKGNINISNVEKVTDNESMVTIENEINGKSEHLISDFKDSFIEKA
                     KEKLTVSPSMRLGFEEFKNASGQIAMGFTEFFGARYDESTLENDPKVVATEKGYSVSV
                     FDKDGNKKDLTSADTFEEAVKLSKEMKHDNSLSRSEIELNQELEKKKI"
     gene            6048. .6365
                     /gene="traB"
                     /locus_tag="VRA0009"
     CDS             6048. .6365
                     /gene="traB"
                     /locus_tag="VRA0009"
                     /note="similar to GP:3676436; identified by sequence
                     similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="TraB"
                     /protein_id="AAQ17132.1"
                     /db_xref="GI:33390926"
                     /translation="MIKKPSLTTVYVAFLSIVLSNITLGAENPGPKIEQGLQQVQTFL
                     TGLIVAVGICAGVWIVLKKLPGIDDPMVKNEMFRGVGMVLAGVAVGAALVWLVPWVYN
                     LFQ"
     gene            6425. .6832
                     /gene="traC"
                     /locus_tag="VRA0010"
     CDS             6425. .6832
                     /gene="traC"
                     /locus_tag="VRA0010"
                     /note="similar to GP:3676437; identified by sequence
                     similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="TraC"
                     /protein_id="AAQ17133.1"
                     /db_xref="GI:33390927"
                     /translation="MSVEQEVKDIMLDMLGEEKKVKENIIPRNVDASYKIFLNLNGKE
                     LAIVFVPFLLFLTIAFGVTFLMGLLNLITGFMVFIVGLIFGLTIYGLLTIRPISTKEN
                     IRMIDTIKQSQRPSRRQKVYFYKSKEGLGDDDV"
     gene            6819. .7502
                     /gene="traD"
                     /locus_tag="VRA0011"
     CDS             6819. .7502
                     /gene="traD"
                     /locus_tag="VRA0011"
                     /note="similar to GP:3676438, and GP:3676438; identified
                     by sequence similarity; putative"

  Query Match             100.0%;  Score 20;  DB 1;  Length 57889;
  Best Local Similarity   100.0%;  Pred. No. 8.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||||
Db      34820 TTCAGGCTCATCCTTCGGTG 34839


RESULT 35
OTPDVANA2
LOCUS       OTPDVANA2                786 bp    DNA     linear   BCT 18-APR-2005
DEFINITION  O.turbata Plasmid DNA for vancomycin resistance protein.
ACCESSION   X79049
VERSION     X79049.1  GI:479085
KEYWORDS    vanA2 gene; vancomycin resistance.
SOURCE      Oerskovia turbata
  ORGANISM  Oerskovia turbata
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Micrococcineae; Cellulomonadaceae; Oerskovia.
REFERENCE   1  (bases 1 to 786)
  AUTHORS   Dutka-Malen,S., Molinas,C., Arthur,M. and Courvalin,P.
  TITLE     The VANA glycopeptide resistance protein is related to
            D-alanyl-D-alanine ligase cell wall biosynthesis enzymes
  JOURNAL   Mol. Gen. Genet. 224 (3), 364-372 (1990)
    PUBMED  2266943
REFERENCE   2
  AUTHORS   Power,E.G., Abdulla,Y.H., Talsania,H.G., Spice,W., Aathithan,S. and
            French,G.L.
  TITLE     vanA genes in vancomycin-resistant clinical isolates of Oerskovia
            turbata and Arcanobacterium (Corynebacterium) haemolyticum
  JOURNAL   J. Antimicrob. Chemother. 36 (4), 595-606 (1995)
    PUBMED  8591934
REFERENCE   3  (bases 1 to 786)
  AUTHORS   Power,E.G.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-APR-1994) E.G.M. Power, UMDS, Dept of Microbiology,
            Guy's Campus, London Bridge, London SE1 9RT, UK
FEATURES             Location/Qualifiers
     source          1. .786
                     /organism="Oerskovia turbata"
                     /mol_type="genomic DNA"
                     /isolate="92"
                     /db_xref="taxon:1713"
     gene            <1. .>786
                     /gene="vanA2"
     CDS             <1. .>786
                     /gene="vanA2"
                     /codon_start=3
                     /transl_table=11
                     /protein_id="CAA55651.1"
                     /db_xref="GI:479086"
                     /db_xref="GOA:Q51332"
                     /db_xref="InterPro:IPR000291"
                     /db_xref="InterPro:IPR011095"
                     /db_xref="InterPro:IPR011127"
                     /db_xref="InterPro:IPR011761"
                     /db_xref="UniProt/TrEMBL:Q51332"
                     /translation="KSGVWKMCEKPCAEWENDNCYSAVLSPDKKMHGLLVKKNHEYEI
                     NHVDVAFSALHGKSGEDGSIQGLFELSGIPFVGCDIQSSAICMDKSLTYIVAKNAGIA
                     TPAFWVINKDDRPVAATSTYPVFGKPARSGSSFGVKKVNSADELDYAIESARQYDSKI
                     LIEQAVSGCEVGCAVLGNSAALVVGEVDQIRLQYGIFRIHQEVEPEKGSENAVITVPA
                     DLSAEERGRIQETGKKIYKALGCRGLARVDMFLQDNGRIVLNE"
     misc_difference 361
                     /gene="vanA2"
                     /note="vanA equilalent position 867"
                     /citation=[1]
                     /replace="t"
     misc_difference 374
                     /gene="vanA2"
                     /note="vanA equivalent position 880"
                     /citation=[1]
                     /replace="t"
     misc_difference 379
                     /gene="vanA2"
                     /note="vanA equivalent position 885"
                     /citation=[1]
                     /replace="t"
     misc_difference 410
                     /gene="vanA2"
                     /note="vanA equivalent position 916"
                     /citation=[1]
                     /replace="t"
     misc_difference 542
                     /gene="vanA2"
                     /note="vanA equivalent position 1048"
                     /citation=[1]
                     /replace="c"
     misc_difference 697
                     /gene="vanA2"
                     /note="vanA equivalent position 1203"
                     /citation=[1]
                     /replace="c"
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 1;  Length 786;
  Best Local Similarity   95.0%;  Pred. No. 58;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          1 TTCAGGCTCATCCTTCGGTG 20
              |||||||||||||||||| |
Db        392 TTCAGGCTCATCCTTCGGGG 411


RESULT 36
AL606928/c
LOCUS       AL606928              186605 bp    DNA     linear   ROD 16-FEB-2002
DEFINITION  Mouse DNA sequence from clone RP23-154F2 on chromosome 3, complete
            sequence.
ACCESSION   AL606928
VERSION     AL606928.9  GI:18855219
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 186605)
  AUTHORS   Corby,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Feb 21, 2002 this sequence version replaced gi:17384520.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-154F2 is
            from the RPCI-23 Mouse PAC Library
            constructed by the group of Pieter de Jong.
            For further details see http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6
            This sequence is the entire insert of clone RP23-154F2 The true
            left end of clone RP23-183J6 is at 140238 in this sequence. The
            true right end of clone RP23-212F17 is at 93544 in this sequence.
FEATURES             Location/Qualifiers
     source          1. .186605
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="3"
                     /clone="RP23-154F2"
                     /clone_lib="RPCI-23"
     misc_feature    4499. .4836
                     /note="Sequence from overlapping clone RP11-212F17
                     (AL583890). Assembly confirmed by restriction digest."
     misc_feature    12403. .12687
                     /note="Sequence from overlapping clone RP11-212F17
                     (AL583890). Assembly confirmed by restriction digest."
     misc_feature    77505
                     /note="Sequence from overlapping clone RP11-212F17
                     (AL583890). Assembly confirmed by restriction digest."
     misc_feature    95115
                     /note="Tandem repeat. Forced join. Gap size estimated to
                     be approximately 40bp by restriction digest data."
     misc_feature    183708
                     /note="Tandem repeat. Forced join. Gap size estimated to
                     be approximately 110bp by restriction digest data."
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 9;  Length 186605;
  Best Local Similarity   95.0%;  Pred. No. 76;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TTCAGGCTCATCCTTCGGTG 20
              |||||||||||||||| ||||
Db     181169 TTCAGGCTCATCCTTGGGTG 181150


RESULT 37
DQ117337/c
LOCUS       DQ117337                399 bp    DNA     linear   ENV 16-JUL-2005
DEFINITION  Uncultured bacterium clone RS.Muc.107 16S ribosomal RNA gene,
            partial sequence.
ACCESSION   DQ117337
VERSION     DQ117337.1  GI:70673105
KEYWORDS    ENV.
SOURCE      uncultured bacterium
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 399)
  AUTHORS   Kushmaro,A., Ben-Dov,E. and Kooperman,N.
  TITLE     Microbial diversity of Fungia granulosa coral mucus micro-layer
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 399)
  AUTHORS   Kushmaro,A., Ben-Dov,E. and Kooperman,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUL-2005) Biotechnology Engineering, Ben Gurion
            University, P.O.B. 653, Be'er-Sheva 84105, Israel
FEATURES             Location/Qualifiers
     source          1. .399
                     /organism="uncultured bacterium"
                     /mol_type="genomic DNA"
                     /isolation_source="coral mucus"
                     /specific_host="Fungia granulosa"
                     /db_xref="taxon:77133"
                     /clone="RS.Muc.107"
                     /environmental_sample
                     /country="Israel: Red Sea"
     rRNA            <1. .>399
                     /product="16S ribosomal RNA"
ORIGIN

  Query Match             90.0%;  Score 18;  DB 3;  Length 399;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||
Db        121 CAGGCTCATCCTTCGGTG 104


RESULT 38
AY327227/c
LOCUS       AY327227                801 bp    DNA     linear   ENV 04-SEP-2003
DEFINITION  Uncultured bacterium clone ZB35 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AY327227
VERSION     AY327227.1  GI:32967957
KEYWORDS    ENV.
SOURCE      uncultured bacterium
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 801)
  AUTHORS   Elshahed,M.S., Senko,J.M., Najar,F.Z., Kenton,S.M., Roe,B.A.,
            Dewers,T.A., Spear,J.R. and Krumholz,L.R.
  TITLE     Bacterial diversity and sulfur cycling in a mesophilic sulfide-rich
            spring
  JOURNAL   Appl. Environ. Microbiol. 69 (9), 5609-5621 (2003)
REFERENCE   2  (bases 1 to 801)
```

```
  AUTHORS   Elshahed,M.S., Senko,J.M., Najar,F.Z., Kenton,S.M., Roe,B.A.,
            Dewers,T.A., Spear,J.R. and Krumholz,L.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUN-2003) Botany and Microbiology, University of
            Oklahoma, 770 Van Vleet Oval, Norman, OK 73019, USA
FEATURES             Location/Qualifiers
     source          1. .801
                     /organism="uncultured bacterium"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:77133"
                     /clone="ZB35"
                     /environmental_sample
     rRNA            <1. .>801
                     /product="16S ribosomal RNA"
ORIGIN

  Query Match             90.0%;  Score 18;  DB 3;  Length 801;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CAGGCTCATCCTTCGGTG 20
              ||||||||||||||||||
Db        230 CAGGCTCATCCTTCGGTG 213


RESULT 39
AY225134
LOCUS       AY225134               48352 bp    DNA     linear   VRL 30-JAN-2004
DEFINITION  Feldmannia irregularis virus a strain FirrV-1 contig B, partial
            sequence.
ACCESSION   AY225134
VERSION     AY225134.1  GI:38683699
KEYWORDS    .
SOURCE      Feldmannia irregularis virus a
  ORGANISM  Feldmannia irregularis virus a
            Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.
REFERENCE   1  (bases 1 to 48352)
  AUTHORS   Delaroque,N., Boland,W., Muller,D.G. and Knippers,R.
  TITLE     Comparisons of two large phaeoviral genomes and evolutionary
            implications
  JOURNAL   J. Mol. Evol. 57 (6), 613-622 (2003)
   PUBMED   14745530
REFERENCE   2  (bases 1 to 48352)
  AUTHORS   Delaroque,N., Knippers,R., Mueller,D.G. and Boland,W.
  TITLE     Partial Nucleotide Sequence of the Feldmannia irregularis Virus
            FirrV-1 Genome: On the Evolution of Large Phaeoviral Genomes
  JOURNAL   Unpublished (2003)
REFERENCE   3  (bases 1 to 48352)
  AUTHORS   Delaroque,N., Knippers,R., Mueller,D.G. and Boland,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2003) Bioorganics, Max Planck Institute for
            Chemical Ecology, Winzerlaer Strasse 10, Jena 07745, Germany
FEATURES             Location/Qualifiers
     source          1. .48352
                     /organism="Feldmannia irregularis virus a"
                     /mol_type="genomic DNA"
                     /strain="FirrV-1"
                     /db_xref="taxon:231992"
                     /clone="contig B"
     CDS             1047. .1343
                     /note="similar to Ectocarpus siliculosus Virus-1 ORF 217;
                     ORF B1"
                     /codon_start=1
                     /product="FirrV-1-B1"
                     /protein_id="AAR26876.1"
                     /db_xref="GI:38683700"
                     /translation="MSTLKERRAVGKLKPLVPLHVKKERDAMRKLKEKKKQAKKEMQE
                     ELYALCKTMLSTVPTISEMKKMTRKDFSAHRKVTNTQWTTLRKYLVRCNHTRFK"
     CDS             complement(1349. .1768)
                     /note="ORF B2"
                     /codon_start=1
                     /product="FirrV-1-B2"
                     /protein_id="AAR26877.1"
                     /db_xref="GI:38683701"
                     /translation="MTDQLKFEDCVPCMPLEDGEKAYVCKVYDGDTCTLAWIDHKGRK
                     VRISCRIRDIDTPEMRSKATEERTRAVQAKEKLADVVLYREVTVKNPGKDKYGRLLAD
                     IATDKLESVAEYMLTFTDLCKPFVKRKTQKNQINIHT"
     CDS             complement(1827. .2249)
                     /note="ORF B3"
                     /codon_start=1
                     /product="FirrV-1-B3"
                     /protein_id="AAR26878.1"
                     /db_xref="GI:38683702"
                     /translation="MDSEKILHRLLGDFGLDGPIRVDGESGLCSVIDVIQLVSQKSKP
                     YARVTFRNVIQDDLQREGGNAPTFSEKIKHVKINNKGHRTPVGNATTIIELIWMLPGR
                     NAMEIARQSAQLVLRYHMGDRELAQQVRTNSFHFKKNI"
     CDS             2370. .4439
                     /note="ORF B4"
                     /codon_start=1
                     /product="FirrV-1-B4"
                     /protein_id="AAR26879.1"
                     /db_xref="GI:38683703"
                     /translation="MSRAQFITPFSLESVFRGELHDEADFRSFVEHRQQSRHRSSEEW
                     RRAWALNRFLCGFLVYTQVLPSYLNGRLKLHQPSEYFCVLDPNSKQHEERKECLRVLQ
                     MAQASEVFDLTGTTSPSLLDFVLRLSVSRPRDCEDLFLKADFRRSKRASAYSVCAATL
                     SHLWFVTTVLGRPCCLESVVLPLRVSEYKSLSMSFPNSLFVRSPPVDWGSLCVPSGYR
                     HECVTGLLLELWAKESHRELFPCEVYTKYKLKCTSRDYVNADCTFSQTMVMVPCYDVV
                     FKNNIVFGRVRHDFSSLLCGKFHELLVVYHEVHQVQRRNTRRFLQVQKSLDPAGIQQK
                     IRKGRMLDPRVESNVTAVKQMIHVMACKIWKGVYEKVRDSIAAEAAEATEATVCREFL
                     KKHRAGEFSCAFSMHEVADVCFLFFLTLCFHRSQVVRDSLVSEYVVSRTGPGYMLSLS
                     RAIKTSGTDCNGVAPVREFELSLSQSMMVHFIKVFGSRSPSDTLLVNERGNTMTQENL
                     CMRFRSMGKEYLGISNLSPHAMRTFFASHAVNSGMVTSANMALFGSYIQVSAKTLSLN
                     YVSASTETEAHVLGKRVLGDVMNCGSSNSSSSSTPAAVVQYKDASNRPNGKVLARARD
                     GFRREMVQSVERFSGNARACFESLVNNRSTSALGDDDKWFEYSNTFFLDHDVRFFLRC
                     ISKKSKN"
     CDS             complement(4436. .5863)
                     /note="ORF B5"
                     /codon_start=1
                     /product="FirrV-1-B5"
                     /protein_id="AAR26880.1"
                     /db_xref="GI:38683704"
                     /translation="MRTVNVLIIGAGPCGLGAATRLHQHGQESWLVVDQADKPGGLSC
                     TEETPEGFLVDKGGHVVFSSFQYFDELLQAALGDYQDESAWATHVRKTHVIMKDSGKY
                     IKVPYPFQHNIGALSCELKHECVEGIVHRDRSRPPHSFKDWVLYNFGQGIARVFMFPY
                     NCKVWAHDLATMSKEWVSARVAHVDSFAVVQNAMNYTECGVWGPNRHFRFPQRGGTGV
                     IYETIARLLPQDKLLLSKKVVGINPETKICTMNDGQSIKYTHLVSTMPLDLLMKQVDM
                     KPDYTLLRHSSTHVLLFGFEGQNPNKQSSWMYFPDEEVPFYRATIFSNYGRYNVPDSA
                     HQYSLMLEVAESQYRKAPADLRTTCLAACRATNLTTASCRLVSEYHERLEYGYPTPTI
                     GLEEYRDKVDEELEKSQIYSRGRFGTYLYQISNQDHSVMQGVQVVDRILFGATETVLR
                     CSEYVNSTYNTQYHYERKPSSSSLV"
     CDS             complement(5879. .6103)
                     /note="ORF B6"
                     /codon_start=1
                     /product="FirrV-1-B6"
                     /protein_id="AAR26881.1"
                     /db_xref="GI:38683705"
                     /translation="MRMCFILIEEDALAAAVLSRDLKYIASSRISARKREKLSALAVG
                     MMTRCALLCFAVLCCTTPSDSFGIAFFFSW"
     misc_feature    complement(5924. .5986)
                     /note="Region: transmembrane domain"
     CDS             6165. .7004
                     /note="ORF B7"
                     /codon_start=1
                     /product="FirrV-1-B7"
                     /protein_id="AAR26882.1"
                     /db_xref="GI:38683706"
                     /translation="MAPKLQVVWHHKVLKETAVGISHALSMMGLEHDLRFLPFSDIED
                     TGDLFIIVGVHHFKKLPANYIVIQVEQAASNWFNASMYGALRGALAVIDFSPRLTTKW
                     AKLGCPFSFYVPIRIPLHPFVGVHPPSVQDIDVLFYGGRRERRVAIEQQLRRALPGRC
                     VLFRYYDLFGAERREKIARSKIVLNLHFWPESSLETHRIEYLLARGACVVSERSSDPV
                     LDAEYEACVTFSEYSSIVSEVVGLLADHERRKDLSRTGYVSVYKRQMNCSHLREAFNS
                     ICN"
     CDS             complement(6985. .7632)
                     /note="ORF B8"
                     /codon_start=1
                     /product="FirrV-1-B8"
```

```
                     /protein_id="AAR26883.1"
                     /db_xref="GI:38683707"
                     /translation="MVNITYHGVTFVVARYKENVEWVRPLVRIFPGTKCFVYNKGTPI
                     DLRDNDITVRQLPNVGRESHTYLTHLLTTAKDADNRVCCVFLQGHPFDHVGTFTQLVR
                     KIRQAILRIAVLGSEFENVGTRLIRIRDFNTTFHPGLKPELIATFHDLFGDKAQRPHE
                     LIFSAGAMFAVSGTVLKPSAFYVKILDWVDKERDPRRGYCLERLWSCIFSSYIYC"
CDS                  7657. .9000
                     /note="ORF B9"
                     /codon_start=1
                     /product="FirrV-1-B9"
                     /protein_id="AAR26884.1"
                     /db_xref="GI:38683708"
                     /translation="MLFFTCHRKKEKKPPPFVEPDLGTSIAETKMKVRMMISCLREIQ
                     LPVKNLMGLTDIIPVMDENSSLHEYAVTINTFGVLLAEMIDNIRLYYQLCSGTYEYVP
                     SDFILLSELRVMWQNLIMKATQKTQRRFFVHRTGDIRCSLTISDNVPNAIVSTDALCL
                     QKVFYAVIYNAIRFTQEGEVKVTVSATNNTGQSQCMLNFIVSDTGIGVPRDFRGILFE
                     PMTKGHSDTVEGGTGMGLAVARLLCRELGGDLVLTDQLTEGSTFHAFILLKCRSIVSW
                     QGSEWHEETTFEFEELPSSRLPSTVTPHIKEDDRQMPRILVVEDIALNREILRHSLNR
                     VHVNVTMSLDGEDAIHKCEEMTYDLILMDIYMPKMNGIDACKKIKQECPLNADTPIVA
                     LSGSTCTDTMKDCLAAGMTEMMVKPISHRVLIKTIYETLTKPEHQQWLTYHDAST"
CDS                  complement(8997. .9752)
                     /note="ORF B10"
                     /codon_start=1
                     /product="FirrV-1-B10"
                     /protein_id="AAR26885.1"
                     /db_xref="GI:38683709"
                     /translation="MSRTHAPQQHPTMAATHFSEFDVSTLKLSPPKTSKANVGCKTAY
                     ITAVGSVKIAIQTPIMTLPWDIVPKKLDDVSNVRAELSLSFVGINEDDPENELKKFKD
                     FLSTFDQKIKTLISETHGAMGKNSEDTRLEASFRDSIKESATGNYPPTIQSKIWLNLK
                     QGGSPSIVEDFDMDVMVFDLEGCQIQTDQMQKGCPAAAILEPSYVWCSALGVGITWVA
                     KQVALQPKSASTFGFNLGKNVAEHEEHEEHEES"
CDS                  complement(9783. .10670)
                     /note="ORF B11"
                     /codon_start=1
                     /product="FirrV-1-B11"
                     /protein_id="AAR26886.1"
                     /db_xref="GI:38683710"
                     /translation="MRDAEILHRAMNNRRVSGPWRATMWRTRDGHVTWVFSEEHENKG
                     ACGLEVQQTDLTSLVAEIIRDTKNVHVFLEHFVHAADVQRTCTTSNSTLQNLRGCLPK
                     GPRIHYIDPRTDLVAILPNGQILEAIVHYAHHLHSQHKDLELKLLLYETFIHPLLSIV
                     SPSGDSAVLEGRLNTVLQKYVANMTTAQMGFFRDKWSVDVIANIENVRRIYHECTTRL
                     SNLPALLEAYTDTVNRFMDLWLLANFFVAENSGMTGSIIYAGSKHSLHFEKYLAEMRY
                     ELLEQFTNRDLSACLALRY"
CDS                  complement(10706. .11050)
                     /note="ORF B12"
                     /codon_start=1
                     /product="FirrV-1-B12 precursor"
                     /protein_id="AAR26887.1"
                     /db_xref="GI:38683711"
                     /translation="MSAVTPEERNFFWTWTRTRYLEDVYTVLALTIWIRAKRYVIELR
                     RVHAVPREVCMIICIHISMKYLGYDELFACRFRDDLLPYYCTMTAKMHEQLEYKILRA
                     LDWTIEDLGVDN"
sig_peptide          complement(10940. .11050)
CDS                  complement(11053. .11259)
                     /note="ORF B13"
                     /codon_start=1
                     /product="FirrV-1-B13 precursor"
                     /protein_id="AAR26888.1"
                     /db_xref="GI:38683712"
                     /translation="MDGTSTGTAGVSLLSGSGLLVESSITLYSGGRSWRFRLPSSSES
                     ENNILVVEYKLGAQWVQAAVYRVP"
sig_peptide          complement(11188. .11259)
CDS                  complement(11298. .12023)
                     /note="ORF B14"
                     /codon_start=1
                     /product="FirrV-1-B14"
                     /protein_id="AAR26889.1"
                     /db_xref="GI:38683713"
                     /translation="MEFLIKWQKQPRQQALEFHKMTGWPTSANVCCHNCCHPFDGVPV
                     PLPYSYDERRRVYLCKGNFCSWQCVKAYNIQDTLVTGKGDRNMYIALLAYKTWYKLTA
                     HTRLATNDGYQALKGYAYTSIQPAQSRENLQMFGGPLSIQEYRRGFFGIMPPDEAFLH
                     PPYVSIRQREKTRDGITPFSLCSASTSPFSRSNGIGTKPREATAGQKENMGMMKRRQK
                     NTDTNTLMSSMGVIVEKKKKEHL"

     CDS             complement(12075. .12596)
                     /note="ORF B15"
                     /codon_start=1
                     /product="FirrV-1-B15"
                     /protein_id="AAR26890.1"
                     /db_xref="GI:38683714"
                     /translation="MDAPTVVLAGLVIVLVVFMLTKNGKHKRDKKPPAPAPSAPTEAE
                     LGSRQRLGGSRLKGIDCDNVALDSPDFARCATTLGARRPNPRLKGEAFPFTEKSGPLE
```

```
  Query Match            87.0%;  Score 17.4;  DB 13;  Length 48352;
  Best Local Similarity  94.7%;  Pred. No. 2.6e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCAGGCTCATCCTTCGGTG 20
              ||||||||||||| ||||||
Db      36373 TCAGGCTCATCCGTCGGTG 36391


RESULT 40
AC131384/c
LOCUS       AC131384               92474 bp    DNA     linear   PRI 24-AUG-2002
DEFINITION  Homo sapiens chromosome 16 clone RP11-465L11, complete sequence.
ACCESSION   AC131384
VERSION     AC131384.1  GI:22380708
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 92474)
  AUTHORS   DOE Joint Genome Institute, Stanford Human Genome Center and Los
            Alamos National Laboratories.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 92474)
  AUTHORS   DOE Joint Genome Institute, Stanford Human Genome Center and Los
            Alamos National Laboratory.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 92474)
  AUTHORS   DOE Joint Genome Institute, Stanford Human Genome Center and Los
            Alamos National Laboratory.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center and Los Alamos
            National Laboratory
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.7% of Sequence;
            Estimated Total Number of Errors is 0.3.
            NOTE:  This is not the entire sequence of the clone (entire
            sequence is 163.3kb).  It is clipped at the overlap with AC091489.
            The number of bases overlapped is 56160.
FEATURES             Location/Qualifiers
     source          1. .92474
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="16"
                     /clone="RP11-465L11"
ORIGIN

  Query Match            87.0%;  Score 17.4;  DB 8;  Length 92474;
  Best Local Similarity  94.7%;  Pred. No. 2.7e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCAGGCTCATCCTTCGGTG 20
              ||||||||||||||| |||
Db      30817 TCAGGCTCATCCTTCAGTG 30799
```

Search completed: April 9, 2006, 07:14:40
Job time : 784.143 secs

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 05:55:33 ; Search time 381.134 Seconds
(without alignments)
472.135 Million cell updates/sec

Title: US-10-661-094-3
Perfect score: 27
Sequence: 1 cctatcctgtttttgttaagccggcgc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27	100.0	27	14	ADY59929	Ady59929 Enterococ
2	27	100.0	1032	4	AAH02300	Aah02300 Enterococ
3	27	100.0	1032	4	AAF76039	Aaf76039 Enterococ
4	27	100.0	1218	4	AAH01064	Aah01064 Enterococ
5	27	100.0	1232	4	AAH01063	Aah01063 Enterococ
6	27	100.0	1237	4	AAH01061	Aah01061 Enterococ
7	27	100.0	1241	4	AAH01058	Aah01058 Enterococ
8	27	100.0	1249	4	AAH01059	Aah01059 Enterococ
9	27	100.0	1263	4	AAH01062	Aah01062 Enterococ
10	27	100.0	1265	4	AAH01065	Aah01065 Enterococ
11	27	100.0	1269	4	AAH01066	Aah01066 Enterococ
12	27	100.0	1272	4	AAH01060	Aah01060 Enterococ
13	27	100.0	1768	4	AAH01148	Aah01148 Enterococ
14	27	100.0	1768	12	ADO47257	Ado47257 E. faeciu
15	27	100.0	1768	14	ADY59927	Ady59927 Enterococ
16	27	100.0	2607	2	AAT28569	Aat28569 Bacterial
17	27	100.0	2607	4	ABA76994	Aba76994 Antibioti
18	27	100.0	3946	4	AAH01150	Aah01150 Enterococ
19	27	100.0	7227	2	AAQ25183	Aaq25183 E.faecium
20	27	100.0	10851	2	AAQ25178	Aaq25178 E.faecium
21	27	100.0	10851	4	AAF76019	Aaf76019 E. faeciu
22	20.8	77.0	1071	8	ACA22997	Aca22997 Prokaryot
23	20.8	77.0	110000	2	AAX20248_07	Continuation (8 of
c 24	20.6	76.3	555	12	ADO47266	Ado47266 Enterococ
c 25	20.6	76.3	556	12	ADO47264	Ado47264 Enterococ
c 26	20.6	76.3	556	12	ADO47262	Ado47262 E. faecal
c 27	20.6	76.3	556	12	ADO47263	Ado47263 E. faecal
c 28	20.6	76.3	556	12	ADO47261	Ado47261 E. faecal
c 29	20.6	76.3	556	12	ADO47265	Ado47265 E. faecal
c 30	20.6	76.3	556	12	ADO47260	Ado47260 E. faecal
c 31	20.6	76.3	556	12	ADO47259	Ado47259 E. faecal
32	20.6	76.3	589	2	AAQ69230	Aaq69230 Enterococ
33	20.6	76.3	630	14	ADY59941	Ady59941 Enterococ
34	20.6	76.3	783	14	ADY59942	Ady59942 Enterococ
35	20.6	76.3	801	4	AAH01126	Aah01126 Enterococ
c 36	20.6	76.3	801	14	ADY59937	Ady59937 Enterococ
c 37	20.6	76.3	801	14	ADY59940	Ady59940 Enterococ
c 38	20.6	76.3	801	14	ADY59943	Ady59943 Consensus
c 39	20.6	76.3	801	14	ADY59939	Ady59939 Enterococ
c 40	20.6	76.3	801	14	ADY59936	Ady59936 Enterococ
c 41	20.6	76.3	801	14	ADY59938	Ady59938 Enterococ
c 42	20.6	76.3	881	12	ADO47258	Ado47258 Enterococ
43	20.6	76.3	1029	2	AAV37115	Aav37115 Antibioti
44	20.6	76.3	1029	4	AAH02303	Aah02303 Enterococ
45	20.6	76.3	1029	4	AAH01720	Aah01720 Enterococ
46	20.6	76.3	1029	4	AAF76048	Aaf76048 Enterococ
47	20.6	76.3	1090	14	ADY59931	Ady59931 Enterococ
48	20.6	76.3	1128	10	ADC90583	Adc90583 E. faeciu
49	20.6	76.3	1141	2	AAQ69235	Aaq69235 Enterococ
50	20.6	76.3	7160	4	AAF76020	Aaf76020 E. faecal
51	20.6	76.3	7678	2	AAX12998	Aax12998 Enterococ
52	20.6	76.3	7678	6	ABS98793	Abs98793 Enterococ
53	19.8	73.3	594	3	AAA38150	Aaa38150 D alanine
54	19.8	73.3	1047	8	ACA48219	Aca48219 Prokaryot
55	19.6	72.6	1191	8	ACA52513	Aca52513 Prokaryot
56	19.6	72.6	21170	2	AAX20535	Aax20535 Polynucle
57	19	70.4	2000	11	ACL36388	Acl36388 Rice stre
58	18.6	68.9	1032	4	AAH01601	Aah01601 Enterococ
59	18.6	68.9	1032	4	AAF76056	Aaf76056 Enterococ
60	18.6	68.9	1280	14	AEB26980	Aeb26980 Pinus rad
61	18.6	68.9	5781	4	AAF76022	Aaf76022 E. faeciu
62	18.2	67.4	774	5	AAS81838	Aas81838 DNA encod
63	18.2	67.4	819	4	AAS52598	Aas52598 E. coli D
64	18.2	67.4	819	13	ADT48822	Adt48822 Bacterial
65	18.2	67.4	1473	13	ADT42360	Adt42360 Bacterial
c 66	18.2	67.4	95109	6	ABQ99654	Abq99654 Human mem
c 67	18	66.7	1206	8	ACA45223	Aca45223 Prokaryot
68	18	66.7	6378	12	ADQ21325	Adq21325 Human sof
69	18	66.7	6502	13	ACN43122	Acn43122 Human dia
70	18	66.7	6592	12	ADQ25197	Adq25197 Human sof
71	17.8	65.9	747	10	ADC81391	Adc81391 Carbonyl
72	17.8	65.9	753	10	ADC81379	Adc81379 Carbonyl
73	17.8	65.9	772	10	ADC81402	Adc81402 Carbonyl
74	17.8	65.9	1158	10	ADC81397	Adc81397 Carbonyl
c 75	17.8	65.9	1394	5	AAS90802	Aas90802 DNA encod
c 76	17.8	65.9	2013	13	ADU00970	Adu00970 DNA encod
c 77	17.8	65.9	2013	13	ADU15352	Adu15352 Novel hum
78	17.8	65.9	88208	14	ADZ13389	Adz13389 Human can
79	17.8	65.9	88445	13	ABD33536	Abd33536 Human can
80	17.8	65.9	121434	12	ADN30326	Adn30326 Human Not
81	17.8	65.9	121434	14	AEA08528	Aea08528 Human Not
82	17.6	65.2	251	12	ADQ06952	Adq06952 Soybean t
83	17.6	65.2	255	12	ADQ06944	Adq06944 Soybean t
84	17.6	65.2	263	12	ADQ06948	Adq06948 Soybean t
85	17.6	65.2	263	12	ADQ06946	Adq06946 Soybean t
86	17.6	65.2	268	12	ADQ06951	Adq06951 Soybean t
87	17.6	65.2	273	12	ADQ06945	Adq06945 Soybean t
c 88	17.6	65.2	277	5	ABV16923	Abv16923 Human pro
89	17.6	65.2	290	12	ADQ06950	Adq06950 Soybean t
c 90	17.6	65.2	430	5	ABV46718	Abv46718 Human pro
c 91	17.6	65.2	525	11	ACH96095	Ach96095 Klebsiell
92	17.6	65.2	943	13	ADX11876	Adx11876 Plant ful

93	17.6	65.2	1026	4	AAS53038	Aas53038 Enterococ
94	17.6	65.2	4948	2	AAT42134	Aat42134 I2C-1 gen
95	17.6	65.2	39982	8	AAD48290	Aad48290 Human enz
96	17.6	65.2	66685	4	AAS07380	Aas07380 Human gen
97	17.6	65.2	66686	6	ABS73149	Abs73149 Human CLA
98	17.4	64.4	318	10	ACF68191	Acf68191 Photorhab
c 99	17.4	64.4	486	4	AAH34587	Aah34587 Human col
c 100	17.4	64.4	747	3	AAZ54529	Aaz54529 Neisseria
c 101	17.4	64.4	754	12	ADO62241	Ado62241 Transcrip
c 102	17.4	64.4	1053	11	ABD12733	Abd12733 Pseudomon
c 103	17.4	64.4	1200	13	ADX60608	Adx60608 Plant ful
c 104	17.4	64.4	1262	12	ADO63288	Ado63288 Transcrip
c 105	17.4	64.4	1310	12	ADO62242	Ado62242 Transcrip
c 106	17.4	64.4	1353	13	ADX53082	Adx53082 Plant ful
107	17.4	64.4	1512	11	ABD12707	Abd12707 Pseudomon
c 108	17.4	64.4	1865	12	ADO62245	Ado62245 Transcrip
109	17.4	64.4	2334	11	ABD12689	Abd12689 Pseudomon
c 110	17.4	64.4	3274	2	AAV17622	Aav17622 Pisum sat
c 111	17.4	64.4	4081	2	AAV06585	Aav06585 Arabidops
c 112	17.4	64.4	23070	9	ADA02507	Ada02507 Mouse Wnt
c 113	17.4	64.4	23070	10	ADB72245	Adb72245 Mouse Wnt
c 114	17.4	64.4	23070	10	ADE95755	Ade95755 Mouse Wnt
c 115	17.4	64.4	23982	14	ADZ12503	Adz12503 Murine ca
116	17.4	64.4	73882	13	ADS73531	Ads73531 tcp gene
c 117	17.4	64.4	110000	10	ACF67367_09	Continuation (10 o
c 118	17.4	64.4	110000	10	ACF65384_3	Continuation (4 of
119	17.4	64.4	111836	13	ABD33102	Abd33102 Murine ca
120	17.4	64.4	256525	11	ACN44148	Acn44148 Mouse gen

ALIGNMENTS

RESULT 1
ADY59929
ID ADY59929 standard; DNA; 27 BP.
XX
AC ADY59929;
XX
DT 02-JUN-2005 (first entry)
XX
DE Enterococcus faecium vanA probe SEQ ID NO:3.
XX
KW DNA detection; antibiotic-resistance; vancomycin; vanA; probe; ss.
XX
OS Enterococcus faecium.
OS Synthetic.
XX
PN US2005058985-A1.
XX
PD 17-MAR-2005.
XX
PF 12-SEP-2003; 2003US-00661094.
XX
PR 12-SEP-2003; 2003US-00661094.
XX
PA (DODG/) DODGSON K J.
XX
PI Dodgson KJ;
XX
DR WPI; 2005-222218/23.
XX
PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX
PS Claim 34; SEQ ID NO 3; 33pp; English.
XX
CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents a
CC probe for Enterococcus faecium vanA, which is used in an example from the
CC present invention.
XX
SQ Sequence 27 BP; 3 A; 8 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 14; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27

RESULT 2
AAH02300
ID AAH02300 standard; DNA; 1032 BP.
XX
AC AAH02300;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecium nucleotide sequence SEQ ID NO:2293.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecium.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Disclosure; Page 1578; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic

CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1032 BP; 303 A; 197 C; 264 G; 268 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 494 CCTATCCTGTTTTTGTTAAGCCGGCGC 520

RESULT 3
AAF76039
ID AAF76039 standard; DNA; 1032 BP.
XX
AC AAF76039;
XX
DT 22-MAY-2001 (first entry)
XX
DE Enterococcus faecium vanA gene, SEQ ID NO:21.
XX
KW Vancomycin resistance reduction; antisense expression inhibition;
KW competitive inducer sequestration; vanH promoter; vanR gene product;
KW Enterococcus; Staphylococcus; Streptococcus; Gram-positive bacterium;
KW antibiotic susceptibility; ex vivo eradication; in vivo eradication;
KW glycopeptide resistance; VanA gene cluster; ds.
XX
OS Enterococcus faecium.
XX
PN WO200112803-A2.
XX
PD 22-FEB-2001.
XX
PF 11-AUG-2000; 2000WO-US022086.
XX
PR 17-AUG-1999; 99US-0149313P.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Inouye RT, Torres-Viera C, Moellering R, Gold H, Eliopoulos GM;
XX
DR WPI; 2001-211216/21.
XX
PT Reducing vancomycin-resistance in vancomycin-resistant organism by
PT introducing a antisense vancomycin-resistance molecule to inhibit
PT vancomycin-resistance gene expression, or by enhancing vanH promoter
PT expression.
XX
PS Example; Page 52; 59pp; English.
XX
CC The invention relates to methods of reducing vancomycin resistance in a
CC vancomycin-resistant organism. One method involves introducing a
CC vancomycin resistance gene antisense nucleic acid into the organism;
CC antisense oligonucleotides complementary to AAF76023-AAF76031 are
CC particularly preferred for this purpose. The second method involves
CC providing additional vanH promoter sequences which are not operatively
CC coupled to a vancomycin resistance gene, so that the phosphorylated vanR
CC gene product (which induces vanH promoter activity) is competitively
CC sequestered. Both methods are able to restore antibiotic susceptibility
CC in glycopeptide resistant enterococci. The methods of the invention are
CC useful for reducing vancomycin resistance in a vancomycin resistant
CC organism, particularly Enterococcus faecium and Enterococcus faecalis,
CC but also in other Gram-positive bacteria such as Staphylococcus sp. and
CC Streptococcus sp., to which Enterococcus faecium and Enterococcus
CC faecalis have the potential to transfer resistance determinants. The
CC antisense molecules are useful in the treatment of infection and
CC colonisation by vancomycin resistant enterococci and other clinically
CC significant pathogens, and may be used for the ex vivo eradication of
CC vancomycin-resistant enterococci from frequently colonised settings, such
CC as intensive care units, haemodialysis units, and chronic care facilities
CC ; for the in vivo clearance of vancomycin- resistant enterococci from
CC colonised gastrointestinal or genitourinary tracts of animals, including
CC humans; and in primary or adjuvant therapy for vancomycin-resistant
CC enterococcal infections. The gene based strategy targets key vancomycin
CC resistance determinants and results in restoration of vancomycin
CC susceptibility in previously glycopeptide- resistant enterococci.
CC Sequences AAF67036-AAF67042 represent genes of the Enterococcus faecium
CC VanA gene cluster
XX
SQ Sequence 1032 BP; 303 A; 197 C; 264 G; 268 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 494 CCTATCCTGTTTTTGTTAAGCCGGCGC 520

RESULT 4
AAH01064
ID AAH01064 standard; DNA; 1218 BP.
XX
AC AAH01064;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus gallinarum nucleotide sequence SEQ ID NO:1055.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus gallinarum.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX

DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 1001-1002; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1218 BP; 364 A; 226 C; 311 G; 317 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 568 CCTATCCTGTTTTTGTTAAGCCGGCGC 594

RESULT 5
AAH01063
ID AAH01063 standard; DNA; 1232 BP.
XX
AC AAH01063;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecalis nucleotide sequence SEQ ID NO:1054.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecalis.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 1001; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1232 BP; 367 A; 228 C; 313 G; 323 T; 0 U; 1 Other;

Query Match 100.0%; Score 27; DB 4; Length 1232;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 578 CCTATCCTGTTTTTGTTAAGCCGGCGC 604

RESULT 6
AAH01061
ID AAH01061 standard; DNA; 1237 BP.
XX
AC AAH01061;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecium nucleotide sequence SEQ ID NO:1052.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecium.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX

PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 999; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1237 BP; 366 A; 235 C; 314 G; 322 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1237;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 590 CCTATCCTGTTTTTGTTAAGCCGGCGC 616

RESULT 7
AAH01058
ID AAH01058 standard; DNA; 1241 BP.
XX
AC AAH01058;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecium nucleotide sequence SEQ ID NO:1049.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecium.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 997; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1241 BP; 371 A; 228 C; 317 G; 325 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1241;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 561 CCTATCCTGTTTTTGTTAAGCCGGCGC 587

RESULT 8
AAH01059
ID AAH01059 standard; DNA; 1249 BP.
XX
AC AAH01059;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus gallinarum nucleotide sequence SEQ ID NO:1050.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;

KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus gallinarum.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 998; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1249 BP; 373 A; 235 C; 316 G; 325 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1249;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 590 CCTATCCTGTTTTTGTTAAGCCGGCGC 616

RESULT 9
AAH01062
ID AAH01062 standard; DNA; 1263 BP.
XX
AC AAH01062;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecium nucleotide sequence SEQ ID NO:1053.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecium.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 1000; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1263 BP; 378 A; 234 C; 321 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1263;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 582 CCTATCCTGTTTTTGTTAAGCCGGCGC 608

RESULT 10
AAH01065
ID AAH01065 standard; DNA; 1265 BP.

XX
AC AAH01065;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecium nucleotide sequence SEQ ID NO:1056.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecium.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 1002; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1265 BP; 379 A; 237 C; 320 G; 329 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1265;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 592 CCTATCCTGTTTTTGTTAAGCCGGCGC 618

RESULT 11
AAH01066
ID AAH01066 standard; DNA; 1269 BP.
XX
AC AAH01066;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus flavescens nucleotide sequence SEQ ID NO:1057.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus flavescens.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 1003; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1269 BP; 380 A; 238 C; 321 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1269;
Best Local Similarity 100.0%; Pred. No. 0.031;

```
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db        590 CCTATCCTGTTTTTGTTAAGCCGGCGC 616


RESULT 12
AAH01060
ID   AAH01060 standard; DNA; 1272 BP.
XX
AC   AAH01060;
XX
DT   24-JUL-2001  (first entry)
XX
DE   Enterococcus faecium nucleotide sequence SEQ ID NO:1051.
XX
KW   Species specific; genus specific; family specific; probe; detection;
KW   identification; algal; archaeal; bacterial; fungal; parasitical;
KW   microorganism; diagnosis; translation elongation factor Tu; toxin;
KW   translation elongation factor G; RecA recombinase; resistance;
KW   catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW   primer; ds.
XX
OS   Enterococcus faecium.
XX
PN   WO200123604-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-CA001150.
XX
PR   28-SEP-1999;   99CA-02283458.
PR   19-MAY-2000; 2000CA-02307010.
XX
PA   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI   Bergeron MG,  Boissinot M,  Huletsky A,  Menard C,  Ouellette M;
PI   Picard FJ,  Roy PH;
XX
DR   WPI; 2001-245006/25.
XX
PT   Nucleic acid sequences are used to generate universal probes and primers
PT   which can be used to identify and detect the presence of algal, archaeal,
PT   bacterial, fungal and parasitical species in a test sample.
XX
PS   Claim 27; Page 998-999; 1580pp; English.
XX
CC   The present invention describes a method for generating a repertory of
CC   nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC   and/or primers are derived. The method comprises amplifying the nucleic
CC   acids of determined algal, archaeal, bacterial, fungal and parasitical
CC   species with a combination of defined primer pairs. The method can be
CC   used for producing probes and/or primers for detecting one or more
CC   related microorganisms e.g. algae, archaea, bacteria, fungi and
CC   parasites, for universal detection and for specific and ubiquitous
CC   detection and identification of an algal, archaeal, bacterial, fungal and
CC   parasitical species, genus, family and group. A nucleic acid (I) obtained
CC   using the method of the invention can be used for the universal detection
CC   of any bacterium, fungus or parasite in a sample and for the detection of
CC   at least one antimicrobial agent resistance gene or at least one toxin
CC   gene. hexA nucleic acids are used for the specific and ubiquitous
CC   detection and for identification of Streptococcus pneumoniae. (I) can be
CC   used to design a therapeutic agent which is effective against
CC   microorganisms. Microbial species or genus or family or phylum or group
CC   which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC   Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC   Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC   gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC   results than substrate specificity tests as results can be determined in
CC   an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC   represent nucleotide sequences and primers/probes which are given in the
CC   exemplification of the present invention
XX
SQ   Sequence 1272 BP; 379 A; 232 C; 325 G; 336 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 27;  DB 4;  Length 1272;
  Best Local Similarity   100.0%;  Pred. No. 0.031;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db        570 CCTATCCTGTTTTTGTTAAGCCGGCGC 596


RESULT 13
AAH01148
ID   AAH01148 standard; DNA; 1768 BP.
XX
AC   AAH01148;
XX
DT   24-JUL-2001  (first entry)
XX
DE   Enterococcus faecium nucleotide sequence SEQ ID NO:1139.
XX
KW   Species specific; genus specific; family specific; probe; detection;
KW   identification; algal; archaeal; bacterial; fungal; parasitical;
KW   microorganism; diagnosis; translation elongation factor Tu; toxin;
KW   translation elongation factor G; RecA recombinase; resistance;
KW   catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW   primer; ds.
XX
OS   Enterococcus faecium.
XX
PN   WO200123604-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-CA001150.
XX
PR   28-SEP-1999;   99CA-02283458.
PR   19-MAY-2000; 2000CA-02307010.
XX
PA   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI   Bergeron MG,  Boissinot M,  Huletsky A,  Menard C,  Ouellette M;
PI   Picard FJ,  Roy PH;
XX
DR   WPI; 2001-245006/25.
XX
PT   Nucleic acid sequences are used to generate universal probes and primers
PT   which can be used to identify and detect the presence of algal, archaeal,
PT   bacterial, fungal and parasitical species in a test sample.
XX
PS   Disclosure; Page 1033-1034; 1580pp; English.
XX
CC   The present invention describes a method for generating a repertory of
CC   nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC   and/or primers are derived. The method comprises amplifying the nucleic
CC   acids of determined algal, archaeal, bacterial, fungal and parasitical
CC   species with a combination of defined primer pairs. The method can be
CC   used for producing probes and/or primers for detecting one or more
CC   related microorganisms e.g. algae, archaea, bacteria, fungi and
CC   parasites, for universal detection and for specific and ubiquitous
CC   detection and identification of an algal, archaeal, bacterial, fungal and
CC   parasitical species, genus, family and group. A nucleic acid (I) obtained
CC   using the method of the invention can be used for the universal detection
CC   of any bacterium, fungus or parasite in a sample and for the detection of
CC   at least one antimicrobial agent resistance gene or at least one toxin
CC   gene. hexA nucleic acids are used for the specific and ubiquitous
CC   detection and for identification of Streptococcus pneumoniae. (I) can be
CC   used to design a therapeutic agent which is effective against
CC   microorganisms. Microbial species or genus or family or phylum or group
CC   which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC   Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC   Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
```

```
CC   gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC   results than substrate specificity tests as results can be determined in
CC   an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC   represent nucleotide sequences and primers/probes which are given in the
CC   exemplification of the present invention
XX
SQ   Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 27;  DB 4;  Length 1768;
  Best Local Similarity   100.0%;  Pred. No. 0.033;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        870 CCTATCCTGTTTTTGTTAAGCCGGCGC 896


RESULT 14
ADO47257
ID   ADO47257 standard; DNA; 1768 BP.
XX
AC   ADO47257;
XX
DT   15-JUL-2004  (first entry)
XX
DE   E. faecium vancomycin resistance gene, vanA.
XX
KW   Vancomycin resistant enterococcus; vancomycin resistance gene; vanA;
KW   gene; ds; hospital acquired infection; VRE;
KW   fluorescence resonance energy transfer; FRET.
XX
OS   Enterococcus faecium.
XX
PN   US2004058336-A1.
XX
PD   25-MAR-2004.
XX
PF   25-SEP-2002; 2002US-00254260.
XX
PR   25-SEP-2002; 2002US-00254260.
XX
PA   (COCK/) COCKERILL F R.
PA   (SLOA/) SLOAN L M.
XX
PI   Cockerill FR,  Sloan LM;
XX
DR   WPI; 2004-268785/25.
XX
PT   Detecting presence or absence of vancomycin-resistant enterococci in
PT   biological sample from individual comprises using real time polymerase
PT   chain reaction.
XX
PS   Disclosure; SEQ ID NO 10; 23pp; English.
XX
CC   The invention relates to detecting the presence or absence of vancomycin-
CC   resistant enterococci (VRE) in a sample, comprising performing a cycling
CC   step by amplifying a sample with pair of vanA or vanB primers and
CC   hybridising the sample with a pair of vanA or vanB probes, labelled with
CC   donor and acceptor fluorescent group, respectively, detecting
CC   fluorescence resonance energy transfer (FRET), where the presence of FRET
CC   indicates presence of VRE. Also included is an article of manufacture,
CC   comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC   and a donor fluorescent group and a corresponding fluorescent group. The
CC   method is useful for detecting the presence or absence of vancomycin-
CC   resistant enterococci in a biological sample, e.g. stool samples, anal or
CC   perirectal swabs, blood and body fluids from an individual. The method
CC   replaces standard culture methods and reduces the cost. The method
CC   provides rapid vancomycin resistant enterococcus real time PCR assay
CC   which is useful for beginning the antimicrobial therapy immediately to
CC   treat hospital acquired infection. The present sequence is an
CC   enterococcal vanA, vancomycin resistance gene.
XX
SQ   Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 27;  DB 12;  Length 1768;
  Best Local Similarity   100.0%;  Pred. No. 0.033;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        870 CCTATCCTGTTTTTGTTAAGCCGGCGC 896


RESULT 15
ADY59927
ID   ADY59927 standard; DNA; 1768 BP.
XX
AC   ADY59927;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Enterococcus faecium vanA DNA sequence SEQ ID NO:1.
XX
KW   DNA detection; antibiotic-resistance; vancomycin; vanA; gene; ds.
XX
OS   Enterococcus faecium.
XX
PN   US2005058985-A1.
XX
PD   17-MAR-2005.
XX
PF   12-SEP-2003; 2003US-00661094.
XX
PR   12-SEP-2003; 2003US-00661094.
XX
PA   (DODG/) DODGSON K J.
XX
PI   Dodgson KJ;
XX
DR   WPI; 2005-222218/23.
XX
PT   Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT   e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT   and/or vanB-specific oligonucleotide probes or primers.
XX
PS   Example 1; SEQ ID NO 1; 33pp; English.
XX
CC   The invention relates to a method for detecting vancomycin resistance
CC   gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC   contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC   probe or primer, and detecting or determining the presence or amount of
CC   hybrid formation or amplified nucleic acid. Also described: (1) an
CC   oligonucleotide composition comprising a first oligonucleotide comprising
CC   sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC   898-917 of the vanA gene, or its complement or portion, or an
CC   oligonucleotide comprising sequences substantially corresponding to
CC   nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC   complement or portion, where the oligonucleotide hybridizes under
CC   stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC   comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC   vanB gene in a test sample, comprising the oligonucleotide mentioned
CC   above. The method and kit are useful for detecting and/or amplifying
CC   genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC   antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC   They may also be used in other industrial purposes, such as for quality
CC   control of food, water, pharmaceutical products or other products
CC   requiring microbiological control. The present sequence represents an
CC   Enterococcus faecium vanA nucleotide sequence from the present invention.
XX
SQ   Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 27;  DB 14;  Length 1768;
  Best Local Similarity   100.0%;  Pred. No. 0.033;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
```

```
                    ||||||||||||||||||||||||||||
Db        870 CCTATCCTGTTTTTGTTAAGCCGGCGC 896

RESULT 16
AAT28569
ID   AAT28569 standard; DNA; 2607 BP.
XX
AC   AAT28569;
XX
DT   01-APR-1997  (first entry)
XX
DE   Bacterial antibiotic resitance gene, vanH, vanA and vanX, probe.
XX
KW   Detection; probe; amplification primer; bacterial pathogen; pneumonia;
KW   Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
KW   Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
KW   Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;
KW   Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
KW   Haemophilus influenzae; Moraxella catarrhalis; septicaemia; meningitis;
KW   infection; intra-abdominal infection; skin infection;
KW   bacterial resistance; beta-lactam antibiotic; ds.
XX
OS   Synthetic.
XX
PN   WO9608582-A2.
XX
PD   21-MAR-1996.
XX
PF   12-SEP-1995;   95WO-CA000528.
XX
PR   12-SEP-1994;   94US-00304732.
XX
PA   (BERG/) BERGERON M G.
PA   (OUEL/) OUELLETTE M.
PA   (ROYP/) ROY P H.
XX
PI   Bergeron MG,  Ouellette M,  Roy PH;
XX
DR   WPI; 1996-179953/18.
XX
PT   Method for the detection of bacterial species using probes and primers -
PT   allows detection and quantification of antibiotic resistant bacteria in
PT   patients, the environment and food.
XX
PS   Claim 94; Page 145-147; 216pp; English.
XX
CC   The sequences given in AAT28560-76 represent fragments derived from
CC   bacterial antibiotic resistance genes which were used as probes in the
CC   method of the invention for the detection of bacterial species in a
CC   sample. The method of the invention comprises using probes and/or
CC   amplification primers which are specific, ubiquitous and sensitive for
CC   determining the presence and/or amount of nucleic acids from selected
CC   bacterial species in any sample, where the bacterial nucleic acid
CC   comprises a selected target region hybridisable with the probes or
CC   primers. The method comprises contacting the sample with the probes or
CC   primers and detecting the presence and/or amount of hybridised primers or
CC   amplification products as and indication of the presence and/or amount of
CC   the bacterial species. This method may be used to detect commonly
CC   encountered bacterial pathogens, e.g. Escherichia coli, Klebsiella
CC   pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis, Streptococcus
CC   pneumoniae, Staphylococcus aureus, Staphylococcus epidermidis,
CC   Enterococcus faecalis, Staphylococcus saprophyticus, Streptococcus
CC   pyogenes, Haemophilus influenzae and Moraxella catarrhalis. These
CC   bacterial species are associated with approx. 90% of urinary tract
CC   infections and with a high percentage of other severe infections
CC   including septicaemia, meningitis, pneumonia, intra-abdominal infections,
CC   skin infections and other severe respiratory tract infections. The method
CC   may also be used to evaluate a bacterial resistance to beta- lactam
CC   antibiotics
XX
SQ   Sequence 2607 BP; 768 A; 506 C; 652 G; 681 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 27;  DB 2;  Length 2607;
  Best Local Similarity   100.0%;  Pred. No. 0.035;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db       1455 CCTATCCTGTTTTTGTTAAGCCGGCGC 1481

RESULT 17
ABA76994
ID   ABA76994 standard; DNA; 2607 BP.
XX
AC   ABA76994;
XX
DT   28-JAN-2002  (first entry)
XX
DE   Antibiotic resistance detection polynucleotide SEQ ID NO 170.
XX
KW   Detection; bacterial species; animal; food; environment;
KW   antibiotic resistance; ds.
XX
OS   Unidentified.
XX
PN   NZ501596-A.
XX
PD   29-JUN-2001.
XX
PF   12-SEP-1995;   95NZ-00501596.
XX
PR   12-SEP-1995;   95NZ-00501596.
XX
PA   (IDII-) IDI INFECTIO DIAGNOSTIC INC.
XX
PI   Bergeron MG,  Ouellette M,  Roy PH;
XX
DR   WPI; 2001-615034/71.
XX
PT   Method for detecting target bacterial species in a sample, comprises
PT   detecting the presence or amount of bacterial nucleic acid amplified by a
PT   primer derived from bacterial DNA, specific for the target bacterial
PT   species.
XX
PS   Claim 16; Page 160-162; 168pp; English.
XX
CC   The invention relates to detecting target bacterial species suspected to
CC   be present in a sample, comprising contacting nucleic acids of target
CC   bacterial species with an amplification primer pair derived from a
CC   bacterial DNA fragment (ABA76825-ABA76861) specific for the target
CC   bacterial species but ubiquitous for different strains, amplifying the
CC   nucleic acid and detecting the presence or amount of an amplified
CC   sequence as an indication of the presence or amount of the target
CC   bacterial species. The invention includes primers and probes (ABA76862-
CC   ABA76984) against the target bacterial species, espeially E.coli,
CC   K.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae, S.aureus,
CC   S.epidermidis, E.faecalis, S.saprophyticus, S.pyogenes, H.influenzae,
CC   M.catarrhalis and/or group A Streptococci producing exotoxin A gene spe
CC   A, suspected to be present in a sample which is obtained from human
CC   patients, animals, environment or food, and which consists of one or more
CC   bacterial colonies. Oligonucleotide probes and primers complementary to
CC   the bacterial genes encoding resistance to antibiotics such as bla(tem),
CC   bla(rob), bla(shv), aadB, aacC1, aacC2, aacC3, aacA4, mecA, vanA, vanH,
CC   vanX, satA, aacA-aphD, vat, vga, msrA, sul and/or int (ABA76985-ABA77001)
CC   are also useful to identify commonly encountered and clinically important
CC   resistance genes. The invention provides a rapid method of bacterial
CC   identification that can be achieved, which reduces the time currently
CC   required for the identification of pathogens in the clinical laboratory
XX
SQ   Sequence 2607 BP; 768 A; 506 C; 652 G; 681 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 27;  DB 4;  Length 2607;
  Best Local Similarity   100.0%;  Pred. No. 0.035;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db       1455 CCTATCCTGTTTTTGTTAAGCCGGCGC 1481
```

```
RESULT 18
AAH01150
ID   AAH01150 standard; DNA; 3946 BP.
XX
AC   AAH01150;
XX
DT   24-JUL-2001  (first entry)
XX
DE   Enterococcus faecium nucleotide sequence SEQ ID NO:1141.
XX
KW   Species specific; genus specific; family specific; probe; detection;
KW   identification; algal; archaeal; bacterial; fungal; parasitical;
KW   microorganism; diagnosis; translation elongation factor Tu; toxin;
KW   translation elongation factor G; RecA recombinase; resistance;
KW   catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW   primer; ds.
XX
OS   Enterococcus faecium.
XX
PN   WO200123604-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-CA001150.
XX
PR   28-SEP-1999;   99CA-02283458.
PR   19-MAY-2000; 2000CA-02307010.
XX
PA   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI   Bergeron MG,  Boissinot M,  Huletsky A,  Menard C,  Ouellette M;
PI   Picard FJ,  Roy PH;
XX
DR   WPI; 2001-245006/25.
XX
PT   Nucleic acid sequences are used to generate universal probes and primers
PT   which can be used to identify and detect the presence of algal, archaeal,
PT   bacterial, fungal and parasitical species in a test sample.
XX
PS   Disclosure; Page 1035-1036; 1580pp; English.
XX
CC   The present invention describes a method for generating a repertory of
CC   nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC   and/or primers are derived. The method comprises amplifying the nucleic
CC   acids of determined algal, archaeal, bacterial, fungal and parasitical
CC   species with a combination of defined primer pairs. The method can be
CC   used for producing probes and/or primers for detecting one or more
CC   related microorganisms e.g. algae, archaea, bacteria, fungi and
CC   parasites, for universal detection and for specific and ubiquitous
CC   detection and identification of an algal, archaeal, bacterial, fungal and
CC   parasitical species, genus, family and group. A nucleic acid (I) obtained
CC   using the method of the invention can be used for the universal detection
CC   of any bacterium, fungus or parasite in a sample and for the detection of
CC   at least one antimicrobial agent resistance gene or at least one toxin
CC   gene. hexA nucleic acids are used for the specific and ubiquitous
CC   detection and for identification of Streptococcus pneumoniae. (I) can be
CC   used to design a therapeutic agent which is effective against
CC   microorganisms. Microbial species or genus or family or phylum or group
CC   which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC   Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC   Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC   gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC   results than substrate specificity tests as results can be determined in
CC   an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC   represent nucleotide sequences and primers/probes which are given in the
CC   exemplification of the present invention
XX
SQ   Sequence 3946 BP; 1235 A; 706 C; 936 G; 1069 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 27;  DB 4;  Length 3946;
  Best Local Similarity  100.0%;  Pred. No. 0.037;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db       1455 CCTATCCTGTTTTTGTTAAGCCGGCGC 1481
```

```
RESULT 19
AAQ25183
ID   AAQ25183 standard; DNA; 7227 BP.
XX
AC   AAQ25183;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   20-NOV-1992  (first entry)
XX
DE   E.faecium antibiotic resistance genes and flanking sequences.
XX
KW   Glycopeptide antibiotic; vancomycin; teicoplanin; resistant;
KW   D-Ala-D-Ala ligase; peptidoglycan precursor; transposon;
KW   inverted repeats; vanR; vanS; vanH; vanA; vanX; ss.
XX
OS   Enterococcus faecium; BM4147.
XX
PN   WO9207942-A1.
XX
PD   14-MAY-1992.
XX
PF   29-OCT-1991;   91WO-FR000855.
XX
PR   31-OCT-1990;   90FR-00013579.
XX
PA   (INSP ) INST PASTEUR.
XX
PI   Arthur M,  Dukta-Malen S,  Molinas C,  Courvalin P;
XX
DR   WPI; 1992-183677/22.
DR   P-PSDB; AAR24305, AAR24306, AAR24307.
XX
PT   Polypeptides involved in expression of glycopeptide antibiotic resistance
PT   - useful in diagnosing presence of Gram-positive enterococcal strains
PT   e.g. Enterococcus Faecium and E Gallinarum.
XX
PS   Disclosure; Fig 4; 163pp; French.
XX
CC   This sequence contains the genes vanH, vanA, vanX, vanR and vanS. The
CC   proteins encoded by the latter two genes (i.e. proteins VanR and VanS)
CC   have a regulatory function and control expression of the other three
CC   ("protective") proteins. See also AAQ25179-Q25182. (Updated on 25-MAR-
CC   2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
CC   (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 7227 BP; 2313 A; 1305 C; 1596 G; 2011 T; 0 U; 2 Other;

  Query Match           100.0%;  Score 27;  DB 2;  Length 7227;
  Best Local Similarity  100.0%;  Pred. No. 0.04;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db       5018 CCTATCCTGTTTTTGTTAAGCCGGCGC 5044
```

```
RESULT 20
AAQ25178
ID   AAQ25178 standard; DNA; 10851 BP.
XX
AC   AAQ25178;
```

```
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   20-NOV-1992  (first entry)
XX
DE   E.faecium antibiotic resistance genes and Tn sequences.
XX
KW   Glycopeptide antibiotic; vancomycin; teicoplanin; resistant;
KW   D-Ala-D-Ala ligase; peptidoglycan precursor; transposon;
KW   inverted repeats; ss.
XX
OS   Enterococcus faecium; BM4147.
XX
FH   Key             Location/Qualifiers
FT   CDS             complement(1. .3189)
FT                   /*tag= a
FT                   /product= "transposase"
FT                   /note= "coded by the (-) strand - see AAQ25179"
FT   repeat_unit     1. .38
FT                   /*tag= j
FT                   /rpt_type= INVERTED
FT   CDS             3187. .3762
FT                   /*tag= b
FT                   /product= "resolvase"
FT   CDS             3976. .4671
FT                   /*tag= c
FT                   /product= "VanR"
FT                   /note= "VanR is a transcription activator"
FT   CDS             4649. .5803
FT                   /*tag= d
FT                   /product= "VanS"
FT                   /note= "VanS is a regulatory protein"
FT   CDS             6018. .6986
FT                   /*tag= e
FT                   /product= "VanH"
FT   CDS             6979. .8010
FT                   /*tag= f
FT                   /product= "VanA"
FT   CDS             8016. .8624
FT                   /*tag= g
FT                   /product= "VanX"
FT   CDS             9052. .9963
FT                   /*tag= h
FT                   /product= "VanY"
FT   CDS             10116. .10601
FT                   /*tag= i
FT                   /product= "VanZ"
FT   repeat_unit     complement(10814. .10851)
FT                   /*tag= k
FT                   /rpt_type= INVERTED
XX
PN   WO9207942-A1.
XX
PD   14-MAY-1992.
XX
PF   29-OCT-1991;   91WO-FR000855.
XX
PR   31-OCT-1990;   90FR-00013579.
XX
PA   (INSP ) INST PASTEUR.
XX
PI   Arthur M,  Dukta-Malen S,  Molinas C,  Courvalin P;
XX
DR   WPI; 1992-183677/22.
DR   P-PSDB; AAR24294, AAR24295, AAR24296, AAR24297, AAR24298, AAR24299,
DR   AAR24300, AAR24301, AAR24302.
XX
PT   Polypeptides involved in expression of glycopeptide antibiotic resistance
PT   - useful in diagnosing presence of Gram-positive enterococcal strains
PT   e.g. Enterococcus Faecium and E Gallinarum.
XX
PS   Claim 9; Fig 8; 163pp; French.
XX
CC   This is a transposon sequence. The transposon comprises the genes
CC   necessary for expression of resistance to glycopeptides in Enterococcus
CC   faecium. It also contains genes associated with resistance, e.g. involved
CC   in regulation of expression of the resistance genes or in the amount of
CC   polypeptides produced. See also AAQ25179-Q25183. (Updated on 25-MAR-2003
CC   to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
CC   (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 10851 BP; 3399 A; 1960 C; 2234 G; 3258 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 27;  DB 2;  Length 10851;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db       7472 CCTATCCTGTTTTTGTTAAGCCGGCGC 7498


RESULT 21
AAF76019
ID   AAF76019 standard; DNA; 10851 BP.
XX
AC   AAF76019;
XX
DT   22-MAY-2001  (first entry)
XX
DE   E. faecium VanA vancomycin resistance gene cluster, SEQ ID NO:1.
XX
KW   Vancomycin resistance reduction; antisense expression inhibition;
KW   competitive inducer sequestration; vanH promoter; vanR gene product;
KW   Enterococcus; Staphylococcus; Streptococcus; Gram-positive bacterium;
KW   antibiotic susceptibility; ex vivo eradication; in vivo eradication;
KW   glycopeptide resistance; VanA gene cluster; ds.
XX
OS   Enterococcus faecium.
XX
PN   WO200112803-A2.
XX
PD   22-FEB-2001.
XX
PF   11-AUG-2000; 2000WO-US022086.
XX
PR   17-AUG-1999;   99US-0149313P.
XX
PA   (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI   Inouye RT,  Torres-Viera C,  Moellering R,  Gold H,  Eliopoulos GM;
XX
DR   WPI; 2001-211216/21.
XX
PT   Reducing vancomycin-resistance in vancomycin-resistant organism by
PT   introducing a antisense vancomycin-resistance molecule to inhibit
PT   vancomycin-resistance gene expression, or by enhancing vanH promoter
PT   expression.
XX
PS   Claim 24; Page 41-44; 59pp; English.
XX
CC   The invention relates to methods of reducing vancomycin resistance in a
CC   vancomycin-resistant organism. One method involves introducing a
CC   vancomycin resistance gene antisense nucleic acid into the organism;
CC   antisense oligonucleotides complementary to AAF76023-AAF76031 are
CC   particularly preferred for this purpose. The second method involves
CC   providing additional vanH promoter sequences which are not operatively
CC   coupled to a vancomycin resistance gene, so that the phosphorylated vanR
CC   gene product (which induces vanH promoter activity) is competitively
CC   sequestered. Both methods are able to restore antibiotic susceptibility
CC   in glycopeptide resistant enterococci. The methods of the invention are
CC   useful for reducing vancomycin resistance in a vancomycin resistant
CC   organism, particularly Enterococcus faecium and Enterococcus faecalis,
CC   but also in other Gram-positive bacteria such as Staphylococcus sp. and
CC   Streptococcus sp., to which Enterococcus faecium and Enterococcus
CC   faecalis have the potential to transfer resistance determinants. The
```

```
CC   antisense molecules are useful in the treatment of infection and
CC   colonisation by vancomycin resistant enterococci and other clinically
CC   significant pathogens, and may be used for the ex vivo eradication of
CC   vancomycin-resistant enterococci from frequently colonised settings, such
CC   as intensive care units, haemodialysis units, and chronic care facilities
CC   ; for the in vivo clearance of vancomycin- resistant enterococci from
CC   colonised gastrointestinal or genitourinary tracts of animals, including
CC   humans; and in primary or adjuvant therapy for vancomycin-resistant
CC   enterococcal infections. The gene based strategy targets key vancomycin
CC   resistance determinants and results in restoration of vancomycin
CC   susceptibility in previously glycopeptide- resistant enterococci. The
CC   present sequence represents the Enterococcus faecium VanA gene cluster
XX
SQ   Sequence 10851 BP; 3392 A; 1962 C; 2237 G; 3260 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 27;  DB 4;  Length 10851;
  Best Local Similarity  100.0%;  Pred. No. 0.042;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db       7472 CCTATCCTGTTTTTGTTAAGCCGGCGC 7498


RESULT 22
ACA22997
ID   ACA22997 standard; DNA; 1071 BP.
XX
AC   ACA22997;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #4654.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Borrelia burgdorferi.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   P-PSDB; ABU19127.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 14; SEQ ID NO 10867; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1071 BP; 335 A; 127 C; 198 G; 411 T; 0 U; 0 Other;

  Query Match            77.0%;  Score 20.8;  DB 8;  Length 1071;
  Best Local Similarity  91.7%;  Pred. No. 21;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTATCCTGTTTTTGTTAAGCCGGC 25
              |||||||||| |||||||||| ||
Db        498 CTATCCTGTTATTGTTAAGCCCGC 521


RESULT 23
AAX20248_07
Continuation (8 of 10) of AAX20248 from base 700001 (Borrelia burgdorferi polynucleotide
WP Sequence split into 10 fragments  LOCUS AAX20248 Accession Aax20248
WP      Fragment Name       Begin      End
WP      AAX20248_00             1    110000
WP      AAX20248_01        100001    210000
WP      AAX20248_02        200001    310000
WP      AAX20248_03        300001    410000
WP      AAX20248_04        400001    510000
WP      AAX20248_05        500001    610000
WP      AAX20248_06        600001    710000
WP      AAX20248_07        700001    810000
WP      AAX20248_08        800001    910000
WP      AAX20248_09        900001    910715

  Query Match            77.0%;  Score 20.8;  DB 2;  Length 110000;
  Best Local Similarity  91.7%;  Pred. No. 41;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTATCCTGTTTTTGTTAAGCCGGC 25
              |||||||||| |||||||||| ||
Db      10177 CTATCCTGTTRTTGTTAAGCCCGC 10200


RESULT 24
ADO47266/c
ID   ADO47266 standard; DNA; 555 BP.
XX
AC   ADO47266;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Enterococcus vancomycin resistance gene, vanB ENEVANB2A.
XX
KW   Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW   gene; ds; hospital acquired infection; VRE;
KW   fluorescence resonance energy transfer; FRET.
```

XX
OS Enterococcus sp.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 20; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 555 BP; 132 A; 161 C; 115 G; 145 T; 0 U; 2 Other;

```
  Query Match             76.3%;  Score 20.6;  DB 12;  Length 555;
  Best Local Similarity   85.2%;  Pred. No. 23;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        391 CCTACCCTGTCTTTGTGAAGCCGGCAC 365
```

RESULT 25
ADO47264/c
ID ADO47264 standard; DNA; 556 BP.
XX
AC ADO47264;
XX
DT 15-JUL-2004 (first entry)
XX
DE Enterococcus vancomycin resistance gene, vanB ENEVANB.
XX
KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW gene; ds; hospital acquired infection; VRE;
KW fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus sp.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 18; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U; 0 Other;

```
  Query Match             76.3%;  Score 20.6;  DB 12;  Length 556;
  Best Local Similarity   85.2%;  Pred. No. 23;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        392 CCTACCCTGTCTTTGTGAAGCCGGCAC 366
```

RESULT 26
ADO47262/c
ID ADO47262 standard; DNA; 556 BP.
XX
AC ADO47262;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU94526.
XX
KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW gene; ds; hospital acquired infection; VRE;
KW fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOA/) SLOAN L M.
XX

PI Cockerill FR, Sloan LM;
XX
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 15; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 133 A; 162 C; 116 G; 145 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
|||| ||||| ||||| |||||||| |
Db 392 CCTACCCTGTCTTTGTGAAGCCGGCAC 366

RESULT 27
ADO47263/c
ID ADO47263 standard; DNA; 556 BP.
XX
AC ADO47263;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU94527.
XX
KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW gene; ds; hospital acquired infection; VRE;
KW fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 17; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
|||| ||||| ||||| |||||||| |
Db 392 CCTACCCTGTCTTTGTGAAGCCGGCAC 366

RESULT 28
ADO47261/c
ID ADO47261 standard; DNA; 556 BP.
XX
AC ADO47261;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU94529.
XX
KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW gene; ds; hospital acquired infection; VRE;
KW fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 14; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with

CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
|||| ||||| ||||| |||||||| |
Db 392 CCTACCCTGTCTTTGTGAAGCCGGCAC 366

RESULT 29
ADO47265/c
ID ADO47265 standard; DNA; 556 BP.
XX
AC ADO47265;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU72704.
XX
KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW gene; ds; hospital acquired infection; VRE;
KW fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 19; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 134 A; 158 C; 117 G; 147 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
|||| ||||| ||||| |||||||| |
Db 392 CCTACCCTGTCTTTGTGAAGCCGGCAC 366

RESULT 30
ADO47260/c
ID ADO47260 standard; DNA; 556 BP.
XX
AC ADO47260;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU94528.
XX
KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW gene; ds; hospital acquired infection; VRE;
KW fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 13; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX

```
SQ   Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;

  Query Match           76.3%;  Score 20.6;  DB 12;  Length 556;
  Best Local Similarity  85.2%;  Pred. No. 23;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        392 CCTACCCTGTCTTTGTGAAGCCGGCAC 366


RESULT 31
ADO47259/c
ID   ADO47259 standard; DNA; 556 BP.
XX
AC   ADO47259;
XX
DT   15-JUL-2004  (first entry)
XX
DE   E. faecalis vancomycin resistance gene, vanB EFU94530.
XX
KW   Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW   gene; ds; hospital acquired infection; VRE;
KW   fluorescence resonance energy transfer; FRET.
XX
OS   Enterococcus faecalis.
XX
PN   US2004058336-A1.
XX
PD   25-MAR-2004.
XX
PF   25-SEP-2002; 2002US-00254260.
XX
PR   25-SEP-2002; 2002US-00254260.
XX
PA   (COCK/) COCKERILL F R.
PA   (SLOA/) SLOAN L M.
XX
PI   Cockerill FR,  Sloan LM;
XX
DR   WPI; 2004-268785/25.
XX
PT   Detecting presence or absence of vancomycin-resistant enterococci in
PT   biological sample from individual comprises using real time polymerase
PT   chain reaction.
XX
PS   Disclosure; SEQ ID NO 16; 23pp; English.
XX
CC   The invention relates to detecting the presence or absence of vancomycin-
CC   resistant enterococci (VRE) in a sample, comprising performing a cycling
CC   step by amplifying a sample with pair of vanA or vanB primers and
CC   hybridising the sample with a pair of vanA or vanB probes, labelled with
CC   donor and acceptor fluorescent group, respectively, detecting
CC   fluorescence resonance energy transfer (FRET), where the presence of FRET
CC   indicates presence of VRE. Also included is an article of manufacture,
CC   comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC   and a donor fluorescent group and a corresponding fluorescent group. The
CC   method is useful for detecting the presence or absence of vancomycin-
CC   resistant enterococci in a biological sample, e.g. stool samples, anal or
CC   perirectal swabs, blood and body fluids from an individual. The method
CC   replaces standard culture methods and reduces the cost. The method
CC   provides rapid vancomycin resistant enterococcus real time PCR assay
CC   which is useful for beginning the antimicrobial therapy immediately to
CC   treat hospital acquired infection. The present sequence is an
CC   enterococcal vanB, vancomycin resistance gene.
XX
SQ   Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;

  Query Match           76.3%;  Score 20.6;  DB 12;  Length 556;
  Best Local Similarity  85.2%;  Pred. No. 23;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        392 CCTACCCTGTCTTTGTGAAGCCGGCAC 366


RESULT 32
AAQ69230
ID   AAQ69230 standard; DNA; 589 BP.
XX
AC   AAQ69230;
XX
DT   25-MAR-2003  (revised)
DT   23-FEB-1995  (first entry)
XX
DE   Enterococcus faecalis vanB gene (internal, amplified fragment).
XX
KW   Gram positive bacteria; inducible glycopeptide resistance; vancomycin;
KW   teicoplanin; antibiotic; vanB gene; ds.
XX
OS   Enterococcus faecalis.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    2. .589
FT                   /*tag= a
FT                   /note= "amplified internal fragment of vanB gene"
XX
PN   FR2699539-A1.
XX
PD   24-JUN-1994.
XX
PF   18-DEC-1992;   92FR-00015671.
XX
PR   18-DEC-1992;   92FR-00015671.
XX
PA   (INSP ) INST PASTEUR.
XX
PI   Arthur M,  Dutka-Malen S,  Evers S,  Courvalin P;
XX
DR   WPI; 1994-227159/28.
DR   P-PSDB; AAR57150.
XX
PT   New protein VanB involved in bacterial resistance to glyco-peptide(s) -
PT   esp vancomycin, and related nucleic acid, vectors, transformed cells and
PT   antibodies, for in vitro detection of resistant strains.
XX
PS   Claim 8; Page 28; 39pp; French.
XX
CC   The protein encoded by the vanB gene is implicated in resistance of Gram-
CC   positive bacteria to glycopeptides, particularly to vancomycin. This
CC   resistance is inducible by Vancomycin but not by teicoplanin. Sequence
CC   AAQ69230 is a claimed internal fragment of the vanB gene. (Updated on 25-
CC   MAR-2003 to correct PN field.)
XX
SQ   Sequence 589 BP; 163 A; 124 C; 166 G; 136 T; 0 U; 0 Other;

  Query Match           76.3%;  Score 20.6;  DB 2;  Length 589;
  Best Local Similarity  85.2%;  Pred. No. 23;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        165 CCTACCCTGTCTTTGTGAAGCCGGCAC 191


RESULT 33
ADY59941
ID   ADY59941 standard; DNA; 630 BP.
XX
AC   ADY59941;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Enterococcus faecalis vanB DNA sequence SEQ ID NO:15.
XX
```

KW DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS Enterococcus faecalis.
XX
PN US2005058985-A1.
XX
PD 17-MAR-2005.
XX
PF 12-SEP-2003; 2003US-00661094.
XX
PR 12-SEP-2003; 2003US-00661094.
XX
PA (DODG/) DODGSON K J.
XX
PI Dodgson KJ;
XX
DR WPI; 2005-222218/23.
XX
PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX
PS Example 1; SEQ ID NO 15; 33pp; English.
XX
CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecalis vanB nucleotide sequence from the present
CC invention.
XX
SQ Sequence 630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 14; Length 630;
Best Local Similarity 85.2%; Pred. No. 24;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        185 CCTACCCTGTCTTTGTGAAGCCGGCAC 211
```

RESULT 34
ADY59942
ID ADY59942 standard; DNA; 783 BP.
XX
AC ADY59942;
XX
DT 02-JUN-2005 (first entry)
XX
DE Enterococcus faecalis vanB DNA sequence SEQ ID NO:16.
XX
KW DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS Enterococcus faecalis.
XX
PN US2005058985-A1.
XX
PD 17-MAR-2005.
XX
PF 12-SEP-2003; 2003US-00661094.
XX
PR 12-SEP-2003; 2003US-00661094.
XX
PA (DODG/) DODGSON K J.
XX
PI Dodgson KJ;
XX
DR WPI; 2005-222218/23.
XX
PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX
PS Example 1; SEQ ID NO 16; 33pp; English.
XX
CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecalis vanB nucleotide sequence from the present
CC invention.
XX
SQ Sequence 783 BP; 215 A; 166 C; 223 G; 179 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 14; Length 783;
Best Local Similarity 85.2%; Pred. No. 24;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        392 CCTACCCTGTCTTTGTGAAGCCGGCAC 418
```

RESULT 35
AAH01126
ID AAH01126 standard; DNA; 801 BP.
XX
AC AAH01126;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecium nucleotide sequence SEQ ID NO:1117.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecium.
XX
PN WO200123604-A2.

XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Disclosure; Page 1027; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 801 BP; 215 A; 169 C; 235 G; 182 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 4; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
|||| ||||| ||||| |||||||| |
Db 389 CCTACCCTGTCTTTGTGAAGCCGGCAC 415

RESULT 36
ADY59937/c
ID ADY59937 standard; DNA; 801 BP.
XX
AC ADY59937;
XX
DT 02-JUN-2005 (first entry)
XX
DE Enterococcus faecium vanB DNA sequence SEQ ID NO:11.
XX
KW DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS Enterococcus faecium.
XX
PN US2005058985-A1.
XX
PD 17-MAR-2005.
XX
PF 12-SEP-2003; 2003US-00661094.
XX
PR 12-SEP-2003; 2003US-00661094.
XX
PA (DODG/) DODGSON K J.
XX
PI Dodgson KJ;
XX
DR WPI; 2005-222218/23.
XX
PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX
PS Example 1; SEQ ID NO 11; 33pp; English.
XX
CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecium vanB nucleotide sequence from the present invention.
XX
SQ Sequence 801 BP; 181 A; 226 C; 169 G; 225 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 14; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
|||| ||||| ||||| |||||||| |
Db 413 CCTACCCTGTCTTTGTGAAGCCGGCAC 387

RESULT 37
ADY59940/c
ID ADY59940 standard; DNA; 801 BP.
XX
AC ADY59940;
XX
DT 02-JUN-2005 (first entry)
XX
DE Enterococcus faecium vanB DNA sequence SEQ ID NO:14.
XX
KW DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS Enterococcus faecium.
XX
PN US2005058985-A1.
XX
PD 17-MAR-2005.
XX
PF 12-SEP-2003; 2003US-00661094.
XX
PR 12-SEP-2003; 2003US-00661094.

```
XX
PA   (DODG/) DODGSON K J.
XX
PI   Dodgson KJ;
XX
DR   WPI; 2005-222218/23.
XX
PT   Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT   e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT   and/or vanB-specific oligonucleotide probes or primers.
XX
PS   Example 1; SEQ ID NO 14; 33pp; English.
XX
CC   The invention relates to a method for detecting vancomycin resistance
CC   gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC   contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC   probe or primer, and detecting or determining the presence or amount of
CC   hybrid formation or amplified nucleic acid. Also described: (1) an
CC   oligonucleotide composition comprising a first oligonucleotide comprising
CC   sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC   898-917 of the vanA gene, or its complement or portion, or an
CC   oligonucleotide comprising sequences substantially corresponding to
CC   nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC   complement or portion, where the oligonucleotide hybridizes under
CC   stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC   comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC   vanB gene in a test sample, comprising the oligonucleotide mentioned
CC   above. The method and kit are useful for detecting and/or amplifying
CC   genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC   antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC   They may also be used in other industrial purposes, such as for quality
CC   control of food, water, pharmaceutical products or other products
CC   requiring microbiological control. The present sequence represents an
CC   Enterococcus faecium vanB nucleotide sequence from the present invention.
XX
SQ   Sequence 801 BP; 183 A; 234 C; 169 G; 215 T; 0 U; 0 Other;

  Query Match            76.3%;  Score 20.6;  DB 14;  Length 801;
  Best Local Similarity  85.2%;  Pred. No. 25;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        413 CCTACCCTGTCTTTGTGAAGCCGGCAC 387


RESULT 38
ADY59943/c
ID   ADY59943 standard; DNA; 801 BP.
XX
AC   ADY59943;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Consensus vanB DNA sequence SEQ ID NO:14.
XX
KW   DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS   Enterococcus faecium.
OS   Enterococcus faecalis.
OS   Synthetic.
XX
PN   US2005058985-A1.
XX
PD   17-MAR-2005.
XX
PF   12-SEP-2003; 2003US-00661094.
XX
PR   12-SEP-2003; 2003US-00661094.
XX
PA   (DODG/) DODGSON K J.
XX
PI   Dodgson KJ;
XX
DR   WPI; 2005-222218/23.
XX
PT   Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT   e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT   and/or vanB-specific oligonucleotide probes or primers.
XX
PS   Example 1; SEQ ID NO 17; 33pp; English.
XX
CC   The invention relates to a method for detecting vancomycin resistance
CC   gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC   contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC   probe or primer, and detecting or determining the presence or amount of
CC   hybrid formation or amplified nucleic acid. Also described: (1) an
CC   oligonucleotide composition comprising a first oligonucleotide comprising
CC   sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC   898-917 of the vanA gene, or its complement or portion, or an
CC   oligonucleotide comprising sequences substantially corresponding to
CC   nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC   complement or portion, where the oligonucleotide hybridizes under
CC   stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC   comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC   vanB gene in a test sample, comprising the oligonucleotide mentioned
CC   above. The method and kit are useful for detecting and/or amplifying
CC   genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC   antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC   They may also be used in other industrial purposes, such as for quality
CC   control of food, water, pharmaceutical products or other products
CC   requiring microbiological control. The present sequence represents a
CC   consensus vanB nucleotide sequence from the present invention.
XX
SQ   Sequence 801 BP; 181 A; 235 C; 169 G; 216 T; 0 U; 0 Other;

  Query Match            76.3%;  Score 20.6;  DB 14;  Length 801;
  Best Local Similarity  85.2%;  Pred. No. 25;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        413 CCTACCCTGTCTTTGTGAAGCCGGCAC 387


RESULT 39
ADY59939/c
ID   ADY59939 standard; DNA; 801 BP.
XX
AC   ADY59939;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Enterococcus faecium vanB DNA sequence SEQ ID NO:13.
XX
KW   DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS   Enterococcus faecium.
XX
PN   US2005058985-A1.
XX
PD   17-MAR-2005.
XX
PF   12-SEP-2003; 2003US-00661094.
XX
PR   12-SEP-2003; 2003US-00661094.
XX
PA   (DODG/) DODGSON K J.
XX
PI   Dodgson KJ;
XX
DR   WPI; 2005-222218/23.
XX
PT   Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT   e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT   and/or vanB-specific oligonucleotide probes or primers.
```

XX
PS Example 1; SEQ ID NO 13; 33pp; English.
XX
CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecium vanB nucleotide sequence from the present invention.
XX
SQ Sequence 801 BP; 183 A; 234 C; 169 G; 215 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 14; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||.|||||.|||||.||||||||.|
Db 413 CCTACCCTGTCTTTGTGAAGCCGGCAC 387

RESULT 40
ADY59936/c
ID ADY59936 standard; DNA; 801 BP.
XX
AC ADY59936;
XX
DT 02-JUN-2005 (first entry)
XX
DE Enterococcus faecium vanB DNA sequence SEQ ID NO:10.
XX
KW DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS Enterococcus faecium.
XX
PN US2005058985-A1.
XX
PD 17-MAR-2005.
XX
PF 12-SEP-2003; 2003US-00661094.
XX
PR 12-SEP-2003; 2003US-00661094.
XX
PA (DODG/) DODGSON K J.
XX
PI Dodgson KJ;
XX
DR WPI; 2005-222218/23.
XX
PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX
PS Example 1; SEQ ID NO 10; 33pp; English.
XX
CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecium vanB nucleotide sequence from the present invention.
XX
SQ Sequence 801 BP; 182 A; 235 C; 169 G; 215 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 14; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||.|||||.|||||.||||||||.|
Db 413 CCTACCCTGTCTTTGTGAAGCCGGCAC 387

Search completed: April 9, 2006, 06:41:33
Job time : 387.134 secs

OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 06:01:49 ; Search time 1049.14 Seconds
(without alignments)
1462.883 Million cell updates/sec

Title: US-10-661-094-3
Perfect score: 27
Sequence: 1 cctatcctgtttttgttaagccggcgc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27	100.0	27	6	CS061875	CS061875 Sequence
2	27	100.0	614	1	AY754011	AY754011 Enterococ
3	27	100.0	1029	6	AR035505	AR035505 Sequence
4	27	100.0	1029	6	BD181846	BD181846 Polypepti
5	27	100.0	1032	1	AY648035	AY648035 Paenibaci
6	27	100.0	1032	1	AY648698	AY648698 Paenibaci
7	27	100.0	1032	6	AX085668	AX085668 Sequence
8	27	100.0	1032	6	AX111560	AX111560 Sequence
9	27	100.0	1034	6	CQ797595	CQ797595 Sequence
10	27	100.0	1218	6	AX110322	AX110322 Sequence
11	27	100.0	1232	6	AX110321	AX110321 Sequence
12	27	100.0	1237	6	AX110319	AX110319 Sequence
13	27	100.0	1241	6	AX110316	AX110316 Sequence
14	27	100.0	1249	6	AX110317	AX110317 Sequence
15	27	100.0	1263	6	AX110320	AX110320 Sequence
16	27	100.0	1265	6	AX110323	AX110323 Sequence
17	27	100.0	1269	6	AX110324	AX110324 Sequence
18	27	100.0	1272	6	AX110318	AX110318 Sequence
19	27	100.0	1768	1	EFPVANAG	X56895 E.faecium p
20	27	100.0	1768	6	CQ797596	CQ797596 Sequence
21	27	100.0	1768	6	CQ797597	CQ797597 Sequence
22	27	100.0	1768	6	CS061873	CS061873 Sequence
23	27	100.0	1768	6	AX110406	AX110406 Sequence
24	27	100.0	2607	6	AR089411	AR089411 Sequence
25	27	100.0	2607	6	AR093611	AR093611 Sequence
26	27	100.0	2667	6	AR035514	AR035514 Sequence
27	27	100.0	2667	6	BD181855	BD181855 Polypepti
28	27	100.0	3946	6	AX110408	AX110408 Sequence
29	27	100.0	4654	1	AY926880	AY926880 Paenibaci
30	27	100.0	7225	6	AR035512	AR035512 Sequence
31	27	100.0	7225	6	BD181853	BD181853 Polypepti
32	27	100.0	9519	1	DQ018711	DQ018711 Paenibaci
33	27	100.0	9537	1	DQ018710	DQ018710 Paenibaci
34	27	100.0	10851	1	TRNVAN	M97297 Enterococcu
35	27	100.0	10851	6	AR035513	AR035513 Sequence
36	27	100.0	10851	6	BD181854	BD181854 Polypepti
37	27	100.0	10851	6	AX085648	AX085648 Sequence
38	27	100.0	17510	1	AF516335	AF516335 Enterococ
39	27	100.0	57889	1	AE017171	AE017171 Staphyloc
40	25.4	94.1	1054	1	BCY15704	Y15704 Bacillus ci
41	23.8	88.1	786	1	OTPDVANA2	X79049 O.turbata P
42	23.8	88.1	9537	1	AF155139	AF155139 Paenibaci
c 43	21.2	78.5	648	10	BV376857	BV376857 S231P613R
c 44	20.8	77.0	12663	1	AE001130	AE001130 Borrelia
c 45	20.8	77.0	110000	1	CP000013_1	Continuation (2 of
c 46	20.8	77.0	110000	1	CP000013_2	Continuation (3 of
47	20.6	76.3	264	1	AY960704	AY960704 Staphyloc
c 48	20.6	76.3	365	1	AY697424	AY697424 Enterococ
49	20.6	76.3	438	1	AY035703	AY035703 Streptoco
50	20.6	76.3	438	1	AY035704	AY035704 Streptoco
51	20.6	76.3	438	1	AY035705	AY035705 Streptoco
52	20.6	76.3	502	1	AY786179	AY786179 Enterococ
c 53	20.6	76.3	556	6	CQ797599	CQ797599 Sequence
c 54	20.6	76.3	556	6	CQ797600	CQ797600 Sequence
c 55	20.6	76.3	556	6	CQ797601	CQ797601 Sequence
c 56	20.6	76.3	556	6	CQ797602	CQ797602 Sequence
c 57	20.6	76.3	556	6	CQ797603	CQ797603 Sequence
c 58	20.6	76.3	556	6	CQ797604	CQ797604 Sequence
c 59	20.6	76.3	556	6	CQ797605	CQ797605 Sequence
c 60	20.6	76.3	556	6	CQ797606	CQ797606 Sequence
61	20.6	76.3	589	1	ENEVANB	L06138 Enterococcu
62	20.6	76.3	589	6	A39314	A39314 Sequence 4
63	20.6	76.3	589	6	AR102788	AR102788 Sequence
64	20.6	76.3	589	6	AR338261	AR338261 Sequence
65	20.6	76.3	630	1	ENEVANB2A	L15304 Enterococcu
66	20.6	76.3	630	6	CS061887	CS061887 Sequence
67	20.6	76.3	635	1	SBVANB2	Z70527 S.bovis bio
c 68	20.6	76.3	671	1	AY704417	AY704417 Enterococ
69	20.6	76.3	732	1	AY665551	AY665551 Enterococ
70	20.6	76.3	783	1	EFU72704	U72704 Enterococcu
71	20.6	76.3	783	6	CS061888	CS061888 Sequence
c 72	20.6	76.3	801	1	EFU94526	U94526 Enterococcu
c 73	20.6	76.3	801	1	EFU94527	U94527 Enterococcu
c 74	20.6	76.3	801	1	EFU94528	U94528 Enterococcu
c 75	20.6	76.3	801	1	EFU94529	U94529 Enterococcu
c 76	20.6	76.3	801	1	EFU94530	U94530 Enterococcu
c 77	20.6	76.3	801	6	CS061882	CS061882 Sequence
c 78	20.6	76.3	801	6	CS061883	CS061883 Sequence
c 79	20.6	76.3	801	6	CS061884	CS061884 Sequence
c 80	20.6	76.3	801	6	CS061885	CS061885 Sequence
c 81	20.6	76.3	801	6	CS061886	CS061886 Sequence
c 82	20.6	76.3	801	6	CS061889	CS061889 Sequence
83	20.6	76.3	801	6	AX110384	AX110384 Sequence
c 84	20.6	76.3	815	1	AY665550	AY665550 Enterococ
c 85	20.6	76.3	882	6	CQ797598	CQ797598 Sequence
86	20.6	76.3	1029	1	AF310953	AF310953 Enterococ
87	20.6	76.3	1029	1	AF310954	AF310954 Enterococ
88	20.6	76.3	1029	1	AF310955	AF310955 Enterococ
89	20.6	76.3	1029	1	AF310957	AF310957 Enterococ
90	20.6	76.3	1029	1	AY145441	AY145441 Enterococ
91	20.6	76.3	1029	1	AY655710	AY655710 Clostridi

92	20.6	76.3	1029	1	AY655711	AY655711 Enterococ
93	20.6	76.3	1029	1	AY655712	AY655712 Clostridi
94	20.6	76.3	1029	1	AY655713	AY655713 Clostridi
95	20.6	76.3	1029	1	AY655714	AY655714 Ruminococ
96	20.6	76.3	1029	1	AY655715	AY655715 Clostridi
97	20.6	76.3	1029	1	AY655716	AY655716 Clostridi
98	20.6	76.3	1029	1	AY655717	AY655717 Clostridi
99	20.6	76.3	1029	1	AY655718	AY655718 Eggerthel
100	20.6	76.3	1029	1	AY655720	AY655720 Clostridi
101	20.6	76.3	1029	1	AY655721	AY655721 Enterococ
102	20.6	76.3	1029	6	AR089432	AR089432 Sequence
103	20.6	76.3	1029	6	AX085677	AX085677 Sequence
104	20.6	76.3	1029	6	AX110980	AX110980 Sequence
105	20.6	76.3	1029	6	AX111563	AX111563 Sequence
106	20.6	76.3	1029	6	BD023048	BD023048 Species-s
107	20.6	76.3	1032	1	AY655719	AY655719 Clostridi
108	20.6	76.3	1045	1	EFA306726	AJ306726 Enterococ
109	20.6	76.3	1045	1	EFA306727	AJ306727 Enterococ
110	20.6	76.3	1063	1	AY958220	AY958220 Enterococ
111	20.6	76.3	1090	1	U00456	U00456 Enterococcu
112	20.6	76.3	1090	6	CS061877	CS061877 Sequence
113	20.6	76.3	1128	6	AR345599	AR345599 Sequence
114	20.6	76.3	1140	6	A39312	A39312 Sequence 2
115	20.6	76.3	1140	6	AR102787	AR102787 Sequence
116	20.6	76.3	1140	6	AR338260	AR338260 Sequence
117	20.6	76.3	1333	1	EFU81452	U81452 Enterococcu
118	20.6	76.3	1333	1	EFVANRES	Z83305 E.faecium v
119	20.6	76.3	4851	1	AF550667	AF550667 Enterococ
120	20.6	76.3	7160	1	EFU35369	U35369 Enterococcu

ALIGNMENTS

```
RESULT 1
CS061875
LOCUS       CS061875                 27 bp    DNA     linear   PAT 13-APR-2005
DEFINITION  Sequence 3 from Patent WO2005028679.
ACCESSION   CS061875
VERSION     CS061875.1  GI:62553769
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Dodgson,K.J.
  TITLE     Method and kit for identifying vancomycin-resistant enterococcus
  JOURNAL   Patent: WO 2005028679-A 3 31-MAR-2005;
            University of Iowa Research Foundation (US); DODGSON, Kirsty Jane
            (US)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match           100.0%;  Score 27;  DB 6;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 0.86;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27


RESULT 2
AY754011
LOCUS       AY754011                 614 bp    DNA     linear   BCT 19-JAN-2005
DEFINITION  Enterococcus faecium vancomycin resistance protein A (vanA) gene,
            partial cds.
ACCESSION   AY754011
VERSION     AY754011.1  GI:57790303
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1  (bases 1 to 614)
  AUTHORS   Khudaier,B.Y., Shafiani,S., Tewari,R. and Taneja,N.
  TITLE     Detection and molecular characterization of vancomycin resistance
            genes from clinical strains of Enterococci
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 614)
  AUTHORS   Khudaier,B.Y., Shafiani,S., Tewari,R. and Taneja,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-SEP-2004) Biotechnology, Panjab University,
            Sector-14, Chandigarh, U.T 160014, India
FEATURES             Location/Qualifiers
     source          1. .614
                     /organism="Enterococcus faecium"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1352"
     gene            <1. .>614
                     /gene="vanA"
     CDS             <1. .>614
                     /gene="vanA"
                     /codon_start=1
                     /transl_table=11
                     /product="vancomycin resistance protein A"
                     /protein_id="AAW56079.1"
                     /db_xref="GI:57790304"
                     /translation="LVKKNHEYEINHVDVAFSALHGKSGEDGSIQGLFELSGIPFVGC
                     DIQSSAICMDKSLTYIVAKNAGIATPAFWVINKDDRPVAATFTYPVFVKPARSGSSFG
                     VKKVNSADELDYAIESARQYDSKILIEQAVSGCEVGCAVLGNSAALAVGEVDQIRLQY
                     GIFRIHQEVEPEKGSENAVITVPADLSAEERGRIQETAKKIYKAL"
ORIGIN

  Query Match           100.0%;  Score 27;  DB 1;  Length 614;
  Best Local Similarity  100.0%;  Pred. No. 0.55;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        260 CCTATCCTGTTTTTGTTAAGCCGGCGC 286


RESULT 3
AR035505
LOCUS       AR035505                 1029 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5871910.
ACCESSION   AR035505
VERSION     AR035505.1  GI:5952173
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1029)
  AUTHORS   Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
  TITLE     Probes for the detection of nucleotide sequences implicated in the
            expression of resistance to glycopeptides, in particular in
            gram-positive bacteria
  JOURNAL   Patent: US 5871910-A 3 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .1029
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           100.0%;  Score 27;  DB 6;  Length 1029;
  Best Local Similarity  100.0%;  Pred. No. 0.51;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
```

```
Db        494 CCTATCCTGTTTTTGTTAAGCCGGCGC 520


RESULT 4
BD181846
LOCUS       BD181846                1029 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Polypeptides implicated in the expression of resistance to
            glycopeptides, in particular in gram-positive bacteria, nucleotide
            sequence cod ing for these polypeptides and use for diagnosis.
ACCESSION   BD181846
VERSION     BD181846.1  GI:30792764
KEYWORDS    JP 2002320494-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1029)
  AUTHORS   Arthur,M., DuktaMmalen,S., Molinas,C. and Courvalin,P.
  TITLE     Polypeptides implicated in the expression of resistance to
            glycopeptides, in particular in gram-positive bacteria, nucleotide
            sequence cod ing for these polypeptides and use for diagnosis
  JOURNAL   Patent: JP 2002320494-A 2 05-NOV-2002;
            INSTITUT PASTEUR
COMMENT     OS   Bacteria
            PN   JP 2002320494-A/2
            PD   05-NOV-2002
            PF   21-FEB-2002 JP 2002045484
            PR   31-OCT-1990 FR     90/13579
            PI   MICHEL ARTHUR,SYLVIE DUKTA-MALEN,CATHERINE MOLINAS,PATRICE  PI
              COURVALIN
            PC   C12N15/09,C07K14/315,C07K16/12,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12Q1/04,C12Q1/68,G01N33/53,G01N33/566,G01N33/569//C12P21/08,
            PC   (C12Q1/04,C12R1:01),(C12Q1/68,C12R1:01),C12N15/00,C12N5/00 CC
             Polypeptides implicated in the expression of resistance to  CC
                  glycopeptides,
            CC   in particular in gram-positive bacteria, nucleotide sequence
            CC            cod ing for
            CC   these polypeptides and use for diagnosis
            FH   Key             Location/Qualifiers
            FT   source          1. .1029
            FT                   /organism='Bacteria'.
FEATURES              Location/Qualifiers
     source           1. .1029
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match           100.0%;  Score 27;  DB 6;  Length 1029;
  Best Local Similarity  100.0%;  Pred. No. 0.51;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        494 CCTATCCTGTTTTTGTTAAGCCGGCGC 520


RESULT 5
AY648035
LOCUS       AY648035                1032 bp    DNA     linear   BCT 29-NOV-2004
DEFINITION  Paenibacillus thiaminolyticus D-alanyl-D-alanine ligase gene,
            complete cds.
ACCESSION   AY648035
VERSION     AY648035.1  GI:50082936
KEYWORDS    .
SOURCE      Paenibacillus thiaminolyticus
  ORGANISM  Paenibacillus thiaminolyticus
            Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
REFERENCE   1  (bases 1 to 1032)
  AUTHORS   Guardabassi,L., Christensen,H., Hasman,H. and Dalsgaard,A.
  TITLE     Members of the Genera Paenibacillus and Rhodococcus Harbor Genes
            Homologous to Enterococcal Glycopeptide Resistance Genes vanA and
            vanB
  JOURNAL   Antimicrob. Agents Chemother. 48 (12), 4915-4918 (2004)
   PUBMED   15561881
REFERENCE   2  (bases 1 to 1032)
  AUTHORS   Guardabassi,L., Hasman,H., Christensen,H. and Dalsgaard,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JUN-2004) Veterinary Pathobiology, The Royal
            Veterinary and Agricultural University, Stigboejlen 4,
            Frederiksberg C 1870, Denmark
FEATURES              Location/Qualifiers
     source           1. .1032
                      /organism="Paenibacillus thiaminolyticus"
                      /mol_type="genomic DNA"
                      /strain="PT-2B1"
                      /db_xref="taxon:49283"
     CDS              1. .1032
                      /codon_start=1
                      /transl_table=11
                      /product="D-alanyl-D-alanine ligase"
                      /protein_id="AAT70090.1"
                      /db_xref="GI:50082937"
                      /translation="MNRVKVAILFGGCSEEHDVSVKSAREIAANIDNEKYEPLYIGIT
                      KFGVWKMCEKPCAEWENSNCYSAVLSPDKKMHGLLVKKNHEYEIHHVDVAFSVLHGKS
                      GEDGSIQGLFELSGIPYVGCDIQSSAICMDKSLTYTIAKNAGIATPDFWVINKDDKPA
                      IDAFTYPVFVKPARSGSSYGVKKVNGADELDAAIESARQYDSKILIEQAVLGCEVGCA
                      VLGNSSELIVGEVDQIRLQHGIFRIHQEAEPEKGSENAVITIPADLSVEVRGRIQETA
                      KKIYKALGCRGLSRVDMFLQDNGSIVLNEVNTLPGFTSYSRYPRMMVAAGITLPELID
                      RLIVLALKG"
ORIGIN

  Query Match           100.0%;  Score 27;  DB 1;  Length 1032;
  Best Local Similarity  100.0%;  Pred. No. 0.51;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        494 CCTATCCTGTTTTTGTTAAGCCGGCGC 520


RESULT 6
AY648698
LOCUS       AY648698                1032 bp    DNA     linear   BCT 29-NOV-2004
DEFINITION  Paenibacillus apiarius D-alanyl-D-alanine ligase gene, complete
            cds.
ACCESSION   AY648698
VERSION     AY648698.1  GI:50082942
KEYWORDS    .
SOURCE      Paenibacillus apiarius
  ORGANISM  Paenibacillus apiarius
            Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
REFERENCE   1  (bases 1 to 1032)
  AUTHORS   Guardabassi,L., Christensen,H., Hasman,H. and Dalsgaard,A.
  TITLE     Members of the Genera Paenibacillus and Rhodococcus Harbor Genes
            Homologous to Enterococcal Glycopeptide Resistance Genes vanA and
            vanB
  JOURNAL   Antimicrob. Agents Chemother. 48 (12), 4915-4918 (2004)
   PUBMED   15561881
REFERENCE   2  (bases 1 to 1032)
  AUTHORS   Guardabassi,L., Hasman,H., Christensen,H. and Dalsgaard,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUN-2004) Veterinary Pathobiology, The Royal
            Veterinary and Agricultural University, Stigboejlen 4,
            Frederiksberg C 1870, Denmark
FEATURES              Location/Qualifiers
     source           1. .1032
                      /organism="Paenibacillus apiarius"
                      /mol_type="genomic DNA"
                      /strain="PA-B2B"
                      /db_xref="taxon:46240"
     CDS              1. .1032
                      /codon_start=1
                      /transl_table=11
                      /product="D-alanyl-D-alanine ligase"
                      /protein_id="AAT70093.1"
```

```
                     /db_xref="GI:50082943"
                     /translation="MYRVKIAILFGGCSEEHDVSVKSAKEIANNINTEKYEPIYIGIT
                     RSGVWKMCEKPCMDWDNENCRSAVLSPDKRMHGLLVMRDKGYQIQRIDAAFSVLHGKS
                     GEDGAIQGLFELSGIPYVGCDIQSSAVCMDKSLAYIIAKNDGIATPEFWVINKDDRPA
                     AAAFTYPVFVKPARSGSSYGVKKVNGADELDAAIESARQYDSKILIEQAVLGCEVGCA
                     VLGNSSELIVGEVDQIRLQHGIFRIHQEAEPEKGSENAVITIPADLSAEERGRIRDTA
                     KKIYKALGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMVAAGITLPELID
                     RLIVLALKG"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 1;  Length 1032;
  Best Local Similarity   100.0%;  Pred. No. 0.51;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        494 CCTATCCTGTTTTTGTTAAGCCGGCGC 520


RESULT 7
AX085668
LOCUS       AX085668               1032 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 21 from Patent WO0112803.
ACCESSION   AX085668
VERSION     AX085668.1  GI:13275654
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Inouye,R.T., Torres-Viera,C., Moellering,R., Gold,H. and
            Eliopoulos,G.M.
  TITLE     Methods and compositions for restoring antibiotic susceptibility in
            glycopeptide-resistant Enterococcus
  JOURNAL   Patent: WO 0112803-A 21 22-FEB-2001;
            Beth Israel Deaconess Medical Center, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1032
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 1032;
  Best Local Similarity   100.0%;  Pred. No. 0.51;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        494 CCTATCCTGTTTTTGTTAAGCCGGCGC 520


RESULT 8
AX111560
LOCUS       AX111560               1032 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 2293 from Patent WO0123604.
ACCESSION   AX111560
VERSION     AX111560.1  GI:13927852
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 2293 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1032
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /strain="BM4147"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 1032;
  Best Local Similarity   100.0%;  Pred. No. 0.51;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        494 CCTATCCTGTTTTTGTTAAGCCGGCGC 520


RESULT 9
CQ797595
LOCUS       CQ797595               1034 bp    DNA     linear   PAT 20-APR-2004
DEFINITION  Sequence 9 from Patent EP1408120.
ACCESSION   CQ797595
VERSION     CQ797595.1  GI:46425887
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Cockerill,F.R. and Sloan,L.M.
  TITLE     Detection of vancomycin-resistant Enterococcus spp
  JOURNAL   Patent: EP 1408120-A 9 14-APR-2004;
            MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .1034
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 1034;
  Best Local Similarity   100.0%;  Pred. No. 0.51;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        494 CCTATCCTGTTTTTGTTAAGCCGGCGC 520


RESULT 10
AX110322
LOCUS       AX110322               1218 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1055 from Patent WO0123604.
ACCESSION   AX110322
VERSION     AX110322.1  GI:13926614
KEYWORDS    .
SOURCE      Enterococcus gallinarum
  ORGANISM  Enterococcus gallinarum
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1055 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1218
                     /organism="Enterococcus gallinarum"
                     /mol_type="unassigned DNA"
                     /strain="R684"
                     /db_xref="taxon:1353"
ORIGIN
```

```
  Query Match            100.0%;  Score 27;  DB 6;  Length 1218;
  Best Local Similarity  100.0%;  Pred. No. 0.5;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        568 CCTATCCTGTTTTTGTTAAGCCGGCGC 594


RESULT 11
AX110321
LOCUS       AX110321               1232 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1054 from Patent WO0123604.
ACCESSION   AX110321
VERSION     AX110321.1  GI:13926613
KEYWORDS    .
SOURCE      Enterococcus faecalis
  ORGANISM  Enterococcus faecalis
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1054 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1232
                     /organism="Enterococcus faecalis"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1351"
                     /note="R610"
ORIGIN

  Query Match            100.0%;  Score 27;  DB 6;  Length 1232;
  Best Local Similarity  100.0%;  Pred. No. 0.5;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        578 CCTATCCTGTTTTTGTTAAGCCGGCGC 604


RESULT 12
AX110319
LOCUS       AX110319               1237 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1052 from Patent WO0123604.
ACCESSION   AX110319
VERSION     AX110319.1  GI:13926611
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1052 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1237
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /strain="R492"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match            100.0%;  Score 27;  DB 6;  Length 1237;
  Best Local Similarity  100.0%;  Pred. No. 0.5;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        590 CCTATCCTGTTTTTGTTAAGCCGGCGC 616


RESULT 13
AX110316
LOCUS       AX110316               1241 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1049 from Patent WO0123604.
ACCESSION   AX110316
VERSION     AX110316.1  GI:13926608
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1049 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1241
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /strain="R690"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match            100.0%;  Score 27;  DB 6;  Length 1241;
  Best Local Similarity  100.0%;  Pred. No. 0.5;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        561 CCTATCCTGTTTTTGTTAAGCCGGCGC 587


RESULT 14
AX110317
LOCUS       AX110317               1249 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1050 from Patent WO0123604.
ACCESSION   AX110317
VERSION     AX110317.1  GI:13926609
KEYWORDS    .
SOURCE      Enterococcus gallinarum
  ORGANISM  Enterococcus gallinarum
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1050 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1249
                     /organism="Enterococcus gallinarum"
                     /mol_type="unassigned DNA"
                     /strain="R691"
                     /db_xref="taxon:1353"
ORIGIN

  Query Match            100.0%;  Score 27;  DB 6;  Length 1249;
  Best Local Similarity  100.0%;  Pred. No. 0.5;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
```

```
Db        590 CCTATCCTGTTTTTGTTAAGCCGGCGC 616


RESULT 15
AX110320
LOCUS       AX110320               1263 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1053 from Patent WO0123604.
ACCESSION   AX110320
VERSION     AX110320.1  GI:13926612
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1053 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1263
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /strain="R581"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 1263;
  Best Local Similarity   100.0%;  Pred. No. 0.5;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        582 CCTATCCTGTTTTTGTTAAGCCGGCGC 608


RESULT 16
AX110323
LOCUS       AX110323               1265 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1056 from Patent WO0123604.
ACCESSION   AX110323
VERSION     AX110323.1  GI:13926615
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1056 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1265
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /strain="R688"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 1265;
  Best Local Similarity   100.0%;  Pred. No. 0.5;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        592 CCTATCCTGTTTTTGTTAAGCCGGCGC 618


RESULT 17
AX110324
LOCUS       AX110324               1269 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1057 from Patent WO0123604.
ACCESSION   AX110324
VERSION     AX110324.1  GI:13926616
KEYWORDS    .
SOURCE      Enterococcus flavescens
  ORGANISM  Enterococcus flavescens
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1057 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1269
                     /organism="Enterococcus flavescens"
                     /mol_type="unassigned DNA"
                     /strain="R689"
                     /db_xref="taxon:37735"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 1269;
  Best Local Similarity   100.0%;  Pred. No. 0.5;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        590 CCTATCCTGTTTTTGTTAAGCCGGCGC 616


RESULT 18
AX110318
LOCUS       AX110318               1272 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1051 from Patent WO0123604.
ACCESSION   AX110318
VERSION     AX110318.1  GI:13926610
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1051 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1272
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /strain="R481"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 1272;
  Best Local Similarity   100.0%;  Pred. No. 0.5;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        570 CCTATCCTGTTTTTGTTAAGCCGGCGC 596


RESULT 19
EFPVANAG
LOCUS       EFPVANAG               1768 bp    DNA     linear   BCT 17-JUN-1991
```

```
DEFINITION  E.faecium plasmid pIP816 vanA gene for VANA ligase.
ACCESSION   X56895
VERSION     X56895.1  GI:43335
KEYWORDS    D-alanyl-D-alanine ligase; VANA glycopeptide resistance protein;
            vancomycin resistance.
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1  (bases 1 to 1768)
  AUTHORS   Dutka-Malen,S., Molinas,C., Arthur,M. and Courvalin,P.
  TITLE     The VANA glycopeptide resistance protein is related to
            D-alanyl-D-alanine ligase cell wall biosynthesis enzymes
  JOURNAL   Mol. Gen. Genet. 224 (3), 364-372 (1990)
   PUBMED   2266943
REFERENCE   2  (bases 1 to 1768)
  AUTHORS   Dutka-Malen,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-FEB-1991) S. Dutka-Malen, Institut Pasteur, Unile des
            Agents Antibacterions, 28 rue du Dr Roux, Paris Cedex 15, France
FEATURES             Location/Qualifiers
     source          1. .1768
                     /organism="Enterococcus faecium"
                     /mol_type="genomic DNA"
                     /strain="BM4147"
                     /db_xref="taxon:1352"
                     /plasmid="pIP816"
     RBS             360. .369
     gene            377. .1408
                     /gene="vanA"
     CDS             377. .1408
                     /gene="vanA"
                     /codon_start=1
                     /evidence=experimental
                     /transl_table=11
                     /product="VANA ligase"
                     /protein_id="CAA40215.1"
                     /db_xref="GI:43336"
                     /db_xref="GOA:P25051"
                     /db_xref="UniProt/Swiss-Prot:P25051"
                     /translation="MNRIKVAILFGGCSEEHDVSVKSAIEIAANINKEKYEPLYIGIT
                     KSGVWKMCEKPCAEWENDNCYSAVLSPDKKMHGLLVKKNHEYEINHVDVAFSALHGKS
                     GEDGSIQGLFELSGIPFVGCDIQSSAICMDKSLTYIVAKNAGIATPAFWVINKDDRPV
                     AATFTYPVFVKPARSGSSFGVKKVNSADELDYAIESARQYDSKILIEQAVSGCEVGCA
                     VLGNSAALVVGEVDQIRLQYGIFRIHQEVEPEKGSENAVITVPADLSAEERGRIQETA
                     KKIYKALGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMAAAGIALPELID
                     RLIVLALKG"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 1;  Length 1768;
  Best Local Similarity   100.0%;  Pred. No. 0.48;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        870 CCTATCCTGTTTTTGTTAAGCCGGCGC 896


RESULT 20
CQ797596
LOCUS       CQ797596                1768 bp    DNA     linear   PAT 20-APR-2004
DEFINITION  Sequence 10 from Patent EP1408120.
ACCESSION   CQ797596
VERSION     CQ797596.1  GI:46425888
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Cockerill,F.R. and Sloan,L.M.
  TITLE     Detection of vancomycin-resistant Enterococcus spp
  JOURNAL   Patent: EP 1408120-A 10 14-APR-2004;
            MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .1768
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1352"
                     /note="vanA sequence"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 1768;
  Best Local Similarity   100.0%;  Pred. No. 0.48;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        870 CCTATCCTGTTTTTGTTAAGCCGGCGC 896


RESULT 21
CQ797597
LOCUS       CQ797597                1768 bp    DNA     linear   PAT 20-APR-2004
DEFINITION  Sequence 11 from Patent EP1408120.
ACCESSION   CQ797597
VERSION     CQ797597.1  GI:46425889
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Cockerill,F.R. and Sloan,L.M.
  TITLE     Detection of vancomycin-resistant Enterococcus spp
  JOURNAL   Patent: EP 1408120-A 11 14-APR-2004;
            MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .1768
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1352"
                     /note="vanA sequence"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 1768;
  Best Local Similarity   100.0%;  Pred. No. 0.48;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        870 CCTATCCTGTTTTTGTTAAGCCGGCGC 896


RESULT 22
CS061873
LOCUS       CS061873                1768 bp    DNA     linear   PAT 13-APR-2005
DEFINITION  Sequence 1 from Patent WO2005028679.
ACCESSION   CS061873
VERSION     CS061873.1  GI:62553767
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Dodgson,K.J.
  TITLE     Method and kit for identifying vancomycin-resistant enterococcus
  JOURNAL   Patent: WO 2005028679-A 1 31-MAR-2005;
            University of Iowa Research Foundation (US); DODGSON, Kirsty Jane
            (US)
FEATURES             Location/Qualifiers
     source          1. .1768
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1352"
```

```
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 1768;
  Best Local Similarity   100.0%;  Pred. No. 0.48;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        870 CCTATCCTGTTTTTGTTAAGCCGGCGC 896


RESULT 23
AX110406
LOCUS       AX110406                1768 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1139 from Patent WO0123604.
ACCESSION   AX110406
VERSION     AX110406.1  GI:13926698
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1139 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .1768
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /strain="BM4147"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 1768;
  Best Local Similarity   100.0%;  Pred. No. 0.48;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db        870 CCTATCCTGTTTTTGTTAAGCCGGCGC 896


RESULT 24
AR089411
LOCUS       AR089411                2607 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 170 from patent US 5994066.
ACCESSION   AR089411
VERSION     AR089411.1  GI:10016168
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2607)
  AUTHORS   Bergeron,M.G., Picard,F.J., Ouellette,M. and Roy,P.H.
  TITLE     Species-specific and universal DNA probes and amplification primers
            to rapidly detect and identify common bacterial pathogens and
            associated antibiotic resistance genes from clinical specimens for
            routine diagnosis in microbiology laboratories
  JOURNAL   Patent: US 5994066-A 170 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .2607
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 2607;
  Best Local Similarity   100.0%;  Pred. No. 0.45;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db       1455 CCTATCCTGTTTTTGTTAAGCCGGCGC 1481


RESULT 25
AR093611
LOCUS       AR093611                2607 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 170 from patent US 6001564.
ACCESSION   AR093611
VERSION     AR093611.1  GI:10020360
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2607)
  AUTHORS   Bergeron,M.G., Ouellette,M. and Roy,P.H.
  TITLE     Species specific and universal DNA probes and amplification primers
            to rapidly detect and identify common bacterial pathogens and
            associated antibiotic resistance genes from clinical specimens for
            routine diagnosis in microbiology laboratories
  JOURNAL   Patent: US 6001564-A 170 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .2607
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 2607;
  Best Local Similarity   100.0%;  Pred. No. 0.45;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db       1455 CCTATCCTGTTTTTGTTAAGCCGGCGC 1481


RESULT 26
AR035514
LOCUS       AR035514                2667 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 17 from patent US 5871910.
ACCESSION   AR035514
VERSION     AR035514.1  GI:5952182
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2667)
  AUTHORS   Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
  TITLE     Probes for the detection of nucleotide sequences implicated in the
            expression of resistance to glycopeptides, in particular in
            gram-positive bacteria
  JOURNAL   Patent: US 5871910-A 17 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .2667
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 2667;
  Best Local Similarity   100.0%;  Pred. No. 0.45;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db       1518 CCTATCCTGTTTTTGTTAAGCCGGCGC 1544


RESULT 27
BD181855
LOCUS       BD181855                2667 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Polypeptides implicated in the expression of resistance to
            glycopeptides, in particular in gram-positive bacteria, nucleotide
```

sequence cod ing for these polypeptides and use for diagnosis.
ACCESSION BD181855
VERSION BD181855.1 GI:30792773
KEYWORDS JP 2002320494-A/11.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 2667)
AUTHORS Arthur,M., DuktaMmalen,S., Molinas,C. and Courvalin,P.
TITLE Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence cod ing for these polypeptides and use for diagnosis
JOURNAL Patent: JP 2002320494-A 11 05-NOV-2002;
INSTITUT PASTEUR
COMMENT OS Bacteria
PN JP 2002320494-A/11
PD 05-NOV-2002
PF 21-FEB-2002 JP 2002045484
PR 31-OCT-1990 FR 90/13579
PI MICHEL ARTHUR,SYLVIE DUKTA-MALEN,CATHERINE MOLINAS,PATRICE PI COURVALIN
PC C12N15/09,C07K14/315,C07K16/12,C12N1/15,C12N1/19,C12N1/21, PC C12N5/10,
PC C12Q1/04,C12Q1/68,G01N33/53,G01N33/566,G01N33/569//C12P21/08,
PC (C12Q1/04,C12R1:01),(C12Q1/68,C12R1:01),C12N15/00,C12N5/00 CC Polypeptides implicated in the expression of resistance to CC glycopeptides,
CC in particular in gram-positive bacteria, nucleotide sequence
CC cod ing for
CC these polypeptides and use for diagnosis
FH Key Location/Qualifiers
FT source 1. .2667
FT /organism='Bacteria'.
FEATURES Location/Qualifiers
source 1. .2667
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 2667;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 1518 CCTATCCTGTTTTTGTTAAGCCGGCGC 1544

RESULT 28
AX110408
LOCUS AX110408 3946 bp DNA linear PAT 29-MAY-2002
DEFINITION Sequence 1141 from Patent WO0123604.
ACCESSION AX110408
VERSION AX110408.1 GI:13926700
KEYWORDS .
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
REFERENCE 1
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M., Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1141 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES Location/Qualifiers
source 1. .3946
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="BM4147"
/db_xref="taxon:1352"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 3946;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 1455 CCTATCCTGTTTTTGTTAAGCCGGCGC 1481

RESULT 29
AY926880
LOCUS AY926880 4654 bp DNA linear BCT 06-MAR-2005
DEFINITION Paenibacillus thiaminolyticus RSA1221 vanA resistance gene cluster, complete sequence.
ACCESSION AY926880
VERSION AY926880.1 GI:60391954
KEYWORDS .
SOURCE Paenibacillus thiaminolyticus
ORGANISM Paenibacillus thiaminolyticus
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
REFERENCE 1 (bases 1 to 4654)
AUTHORS Moodley,A., van Nierop,W. and Marais,E.
TITLE Paenibacillus thiaminolyticus RSA1221 vanA resistance gene cluster
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4654)
AUTHORS Moodley,A., van Nierop,W. and Marais,E.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2005) Clinical Microbiology and Infectious Diseases, University of the Witwatersrand, 7 York Road, Parktown, Johannesburg, Gauteng 2193, South Africa
FEATURES Location/Qualifiers
source 1. .4654
/organism="Paenibacillus thiaminolyticus"
/mol_type="genomic DNA"
/strain="RSA1221"
/db_xref="taxon:49283"
gene 1. .696
/gene="vanR"
CDS 1. .696
/gene="vanR"
/codon_start=1
/transl_table=11
/product="transcriptional response regulator"
/protein_id="AAX19281.1"
/db_xref="GI:60391955"
/translation="MSDKILIVDDEHEIADLVELYLKNENYTVFKYYTAKEALECIDK
SEIDLAILDIMLPGTSGLTICQKIRDKHTYPIIMLTGKDTEVDKITGLTIGADDYITK
PFRPLELIARVKAQLRRYKKFSGVKEQNENVIVHSGLVINVNTHECYLNEKQLSLTPT
EFSILRILCENKGNVVSSELLFHEIWGDEYFSKSNNTITVHIRHLREKMNDTIDNPKY
IKTVWGVGYKIEK"
gene 674. .1834
/gene="vanS"
CDS 674. .1834
/gene="vanS"
/codon_start=1
/transl_table=11
/product="histidine protein kinase"
/protein_id="AAX19282.1"
/db_xref="GI:60391956"
/translation="MAIKLKNKNKKTDYSKLKRKLYQYIVVIVMAAVVFVLFLRLFIK
GTLGEWIVRFLENSYHLDRLDAMKLYQYSIRNNIDIFIYVAIVISILILCRVMLSKFA
KYFDEINTGIDVLIQNEDKQIELSAEMDVMEQKLNTLKRTLEKREQDAKLAEQRKNDV
VMYLAHDIKTPLTSIIGYLSLLDEAPDMPVDQKAKYVHITLDKAYRLEQLIDEFFEIT
RYNLQTITLTKTHIDLYYMLVQMTDEFYPQLSAHGKQAVIHAPEDLTVSGDPDKLARV
FNNILENAAAYSEDNSVIDITAGLSGDVVSIVFKNAGSIPKDKLAAIFEKFYRLDDAR
SSDTGGAGLGLAIAKEIIVQHGGQIYAESNDNYTTFTVELPALPDLVDKRSS"
gene 2048. .3016
/gene="vanH"
CDS 2048. .3016
/gene="vanH"
/codon_start=1

```
                     /transl_table=11
                     /product="D-specific dehydrogenase"
                     /protein_id="AAX19283.1"
                     /db_xref="GI:60391957"
                     /translation="MNNIGITVYGCEQDEADAFCALSPRFGVMPSIINANVSESNAKS
                     APFNQCISVGHKSEVSASILLALKRAGVKYISTRSIGCNHIDTTAAKRMGITVGNVAY
                     SPDSVADYTMMLMLMAVRNAKSIVRSVEKHDFRLDSVRGKVLSDMTVGVVGTGHIGKA
                     VIERLRGFGCKVLAYSRSQSIEANYVPFDELLQNSDIVTLHVPLNADTRHIISHEQIQ
                     RMKQGAFIINTGRGPLVYTNELVKALENGKLGGAALDVLEGEEEFFYSDCSQKPIDNQ
                     FLLKLQRMPNVIITPHTAFYTEQALRDTVEKTNINCLDFERSQEHE"
     gene            3009. .4040
                     /gene="vanA"
     CDS             3009. .4040
                     /gene="vanA"
                     /codon_start=1
                     /transl_table=11
                     /product="D-alanine:D-lactate ligase"
                     /protein_id="AAX19284.1"
                     /db_xref="GI:60391958"
                     /translation="MNRVKVAILFGGCSEEHDVSVKSAREIAANIDNEKYEPLYIGIT
                     KSGVWKMCEKPCAEWENSNCYSAVLSPDKKMHGLLVKKNHEYEIHHVDVAFSGMHSKS
                     GEDGSIQGLFELSGIPYVGCDIQSSAICMDKSLTYTIAKNAGIAIPEFWVINKDDKPA
                     ADTFTYPVFVKPARSGSSYGVKKVNVADELDAAIESARQYDSKILIEQAVLGCEVGCA
                     VLGNSSELIVGEVDQIRLQHGIFRIHQEAEPEKGSENAVITIPADLSAEERGRIQETA
                     KKIYKALGCRGLSRVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMAAAGITLPELID
                     RLIVFALQG"
     gene            4046. .4654
                     /gene="vanX"
     CDS             4046. .4654
                     /gene="vanX"
                     /codon_start=1
                     /transl_table=11
                     /product="D,D-dipeptidase"
                     /protein_id="AAX19285.1"
                     /db_xref="GI:60391959"
                     /translation="MKKGFTFLDEILHGVRWDAKYATWDNFTGKPVDGYEVNRIAGTY
                     ELADALLKVKELAAAQGYGLLLWDGYRPQRAVNCFVQWAAQPEDGLTKERYYPNIDRT
                     EMVSKGYVASKSSHSRGSAIDLTLYRLDTGELVPMGSGFDFMDERSHHAAKGISGNEA
                     QNRRCLRSIMENSGFEAYSFEWWHYVLRNEPYPNSYFDFPVK"
ORIGIN

  Query Match           100.0%;  Score 27;  DB 1;  Length 4654;
  Best Local Similarity  100.0%;  Pred. No. 0.42;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db       3502 CCTATCCTGTTTTTGTTAAGCCGGCGC 3528


RESULT 30
AR035512
LOCUS       AR035512                7225 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 15 from patent US 5871910.
ACCESSION   AR035512
VERSION     AR035512.1  GI:5952180
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7225)
  AUTHORS   Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
  TITLE     Probes for the detection of nucleotide sequences implicated in the
            expression of resistance to glycopeptides, in particular in
            gram-positive bacteria
  JOURNAL   Patent: US 5871910-A 15 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .7225
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           100.0%;  Score 27;  DB 6;  Length 7225;
  Best Local Similarity  100.0%;  Pred. No. 0.39;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db       5016 CCTATCCTGTTTTTGTTAAGCCGGCGC 5042


RESULT 31
BD181853
LOCUS       BD181853                7225 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Polypeptides implicated in the expression of resistance to
            glycopeptides, in particular in gram-positive bacteria, nucleotide
            sequence cod ing for these polypeptides and use for diagnosis.
ACCESSION   BD181853
VERSION     BD181853.1  GI:30792771
KEYWORDS    JP 2002320494-A/9.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 7225)
  AUTHORS   Arthur,M., DuktaMmalen,S., Molinas,C. and Courvalin,P.
  TITLE     Polypeptides implicated in the expression of resistance to
            glycopeptides, in particular in gram-positive bacteria, nucleotide
            sequence cod ing for these polypeptides and use for diagnosis
  JOURNAL   Patent: JP 2002320494-A 9 05-NOV-2002;
            INSTITUT PASTEUR
COMMENT     OS   Bacteria
            PN   JP 2002320494-A/9
            PD   05-NOV-2002
            PF   21-FEB-2002 JP 2002045484
            PR   31-OCT-1990 FR     90/13579
            PI   MICHEL ARTHUR,SYLVIE DUKTA-MALEN,CATHERINE MOLINAS,PATRICE  PI
              COURVALIN
            PC   C12N15/09,C07K14/315,C07K16/12,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12Q1/04,C12Q1/68,G01N33/53,G01N33/566,G01N33/569//C12P21/08,
            PC   (C12Q1/04,C12R1:01),(C12Q1/68,C12R1:01),C12N15/00,C12N5/00 CC
             Polypeptides implicated in the expression of resistance to  CC
                glycopeptides,
            CC   in particular in gram-positive bacteria, nucleotide sequence
            CC            cod ing for
            CC   these polypeptides and use for diagnosis
            FH   Key             Location/Qualifiers
            FT   source          1. .7225
            FT                   /organism='Bacteria'.
FEATURES             Location/Qualifiers
     source          1. .7225
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match           100.0%;  Score 27;  DB 6;  Length 7225;
  Best Local Similarity  100.0%;  Pred. No. 0.39;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db       5016 CCTATCCTGTTTTTGTTAAGCCGGCGC 5042


RESULT 32
DQ018711
LOCUS       DQ018711                9519 bp    DNA     linear   BCT 31-MAY-2005
DEFINITION  Paenibacillus apiarius strain PA-B2B glycopeptide resistance vanA
            operon, complete sequence; and BtrU-like protein gene, partial cds.
ACCESSION   DQ018711
VERSION     DQ018711.1  GI:66731642
KEYWORDS    .
SOURCE      Paenibacillus apiarius
  ORGANISM  Paenibacillus apiarius
            Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
```

```
REFERENCE   1  (bases 1 to 9519)
  AUTHORS   Guardabassi,L., Perichon,B., Van Heijenoort,J., Blanot,D. and
            Courvalin,P.
  TITLE     Glycopeptide resistance van operons in Paenibacillus from soil
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 9519)
  AUTHORS   Guardabassi,L., Perichon,B., Van Heijenoort,J., Blanot,D. and
            Courvalin,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-APR-2005) Unite des Agents Antibacteriens, Institut
            Pasteur, 25 rue du Docteur Roux, Paris 75015, France
FEATURES             Location/Qualifiers
     source          1. .9519
                     /organism="Paenibacillus apiarius"
                     /mol_type="genomic DNA"
                     /strain="PA-B2B"
                     /isolation_source="soil"
                     /db_xref="taxon:46240"
     operon          1. .7648
                     /operon="glycopeptide resistance vanA"
     gene            1. .696
                     /gene="vanR"
                     /operon="glycopeptide resistance vanA"
     CDS             1. .696
                     /gene="vanR"
                     /operon="glycopeptide resistance vanA"
                     /note="response regulator"
                     /codon_start=1
                     /transl_table=11
                     /product="VanR"
                     /protein_id="AAY52009.1"
                     /db_xref="GI:66731643"
                     /translation="MSDKILVVDDEHEIADLVELYLKNENYTVFKYYTAKEALECIDK
                     TDLDLAILDIMLPGASGLAICQKIRDKHTYPIITLTAKDTEVDKITGLTIGADDYITK
                     PFRPLELIARVKAQLRRYKKYNGVTEQNENVIVHSGLVININTHECFLNEKQLSLTPT
                     EFSILRILCENKGNVVSSEQLFHEIWGDEYFSKSNNTITVHIRHLREKMNDTIDNPKY
                     IKTVWGVGYKIEK"
     gene            674. .1840
                     /gene="vanS"
                     /operon="glycopeptide resistance vanA"
     CDS             674. .1840
                     /gene="vanS"
                     /operon="glycopeptide resistance vanA"
                     /note="sensor histidine kinase"
                     /codon_start=1
                     /transl_table=11
                     /product="VanS"
                     /protein_id="AAY52010.1"
                     /db_xref="GI:66731644"
                     /translation="MAIKLKNKNKNKKTDYSKLKRKLYQYIVVIVMAAAVFVLFLRLF
                     IKGTLGEWIVRFLENSYHLERQDAMIIYQYTIRNNIEIFIYVAIAISILILCRVMLSK
                     FAKYFDEINTGIDILIQNEDKQIELSAEMEFMEQKLNTLKRTLEKREQDAKLAEQRKN
                     DVVMYLAHDIKTPLTSVIGYLSLLDEAPDMPVEQKAKYVHITLDKAYRLEQLIDEFFE
                     ITRYNLQTITLTKKHIDLYYMLVQMADEFYPQLAANGKQAVIHASEDLTVTGDSDKLA
                     RVFNNILKNAAAYSEDNSVIDITAGLSGDVVSIVFKNAGSIPKDKLAAIFEKFYRLDD
                     ARSSDTGGAGLGLAIAKGIIVQHGGQIYAESNDNYTTFTVELPALPDLVDKRSS"
     gene            2047. .2862
                     /gene="vanW"
                     /operon="glycopeptide resistance vanA"
     CDS             2047. .2862
                     /gene="vanW"
                     /operon="glycopeptide resistance vanA"
                     /codon_start=1
                     /transl_table=11
                     /product="VanW-like protein"
                     /protein_id="AAY52011.1"
                     /db_xref="GI:66731645"
                     /translation="MTQIFPPLLPVRVMQRKMCFYAGMRFDGRRYAETIDGKQLPYKL
                     FEAGCALYNGNTGFDMAYQENKVFNLKLAAKTLNGLLIRPGETFSFWRLVRHADKHIP
                     YKDGLTVTNGKLTTAPGGGLCQMSNLLFWMFLHTPLTVTERSGHEVKEFPEPNSDEIK
                     GVDATISEGWIDLKARNGTDCTYQISVAFDDENIIGTVFVDKRPQVLYRVANGGIEYS
                     RESGGIYESVKVERAEIDSDTGEITGQKPLYTNKCKICYPLPENVEIKEAKKV"
     gene            3168. .4136
                     /gene="vanH"
                     /operon="glycopeptide resistance vanA"
     CDS             3168. .4136
                     /gene="vanH"
                     /operon="glycopeptide resistance vanA"
                     /note="deydrogenase"
                     /codon_start=1
                     /transl_table=11
                     /product="VanH"
                     /protein_id="AAY52012.1"
                     /db_xref="GI:66731646"
                     /translation="MKNIGITIYGCEQDEADVFKELSPRFGVIPAITSSAVSETNVML
                     APGNQCISVGHKSEISESILLALKESGVKYISTRSIGYNHIDMKAAESMGIAVGNVAY
                     SPDSVADYTLMLMLMAVRNAKSIVRSVEKHDFKLDSVRGKVLRDMTVGVLGTGHIGKR
                     VIERLRGFGCHVLAYGHNKEAAANYVSLNELLQKSDILTIHVPLSADTYHMIGREQIK
                     AMKQGAFLINTARGGLIDTDVLVKALENGKLGGAALDVLEGEEGLFYFDCTQKPIDNQ
                     FLLKLQRMPNVIITPHTAYYTEQALRDTVENTIKNCLEFERRETLV"
     gene            4129. .5160
                     /gene="vanA"
                     /operon="glycopeptide resistance vanA"
     CDS             4129. .5160
                     /gene="vanA"
                     /operon="glycopeptide resistance vanA"
                     /note="D-Ala:D-Lac ligase"
                     /codon_start=1
                     /transl_table=11
                     /product="VanA"
                     /protein_id="AAY52016.1"
                     /db_xref="GI:66731650"
                     /translation="MYRVKIAILFGGCSEEHDVSVKSAKEIANNINTEKYEPIYIGIT
                     RSGVWKMCEKPCMDWDNENCRSAVLSPDKRMHGLLVMRDKGYQIQRIDAAFSVLHGKS
                     GEDGAIQGLFELSGIPYVGCDIQSSAVCMDKSLAYIIAKNDGIATPEFWVINKDDRPA
                     AAAFTYPVFVKPARSGSSYGVKKVNGADELDAAIESARQYDSKILIEQAVLGCEVGCA
                     VLGNSSELIVGEVDQIRLQHGIFRIHQEAEPEKGSENAVITIPADLSAEERGRIRDTA
                     KKIYKALGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMVAAGITLPELID
                     RLIVLALKG"
     gene            5166. .5750
                     /gene="vanX"
                     /operon="glycopeptide resistance vanA"
     CDS             5166. .5750
                     /gene="vanX"
                     /operon="glycopeptide resistance vanA"
                     /note="D,D-dipeptidase"
                     /codon_start=1
                     /transl_table=11
                     /product="VanX"
                     /protein_id="AAY52017.1"
                     /db_xref="GI:66731651"
                     /translation="MEKGFVFLDEILHGVRWDAKYATWDNFTGKPVDGYEVNRIVGTH
                     ALALALLKAQKQAAALGYGLLLWDGYRPKRAVDCFLRWSEQPEDNLTKERYYPNIERT
                     EMVSKGYVASKSSHSRGSAIDLTLYRLDTGELVPMGSGFDFMDERSHHAAKGIASMEA
                     QNRRRLRSIMENSGFEPYSFEWWHYVLRNETIPQ"
     gene            6234. .7133
                     /gene="vanY"
                     /operon="glycopeptide resistance vanA"
     CDS             6234. .7133
                     /gene="vanY"
                     /operon="glycopeptide resistance vanA"
                     /note="D,D-carboxypeptidase"
                     /codon_start=1
                     /transl_table=11
                     /product="VanY"
                     /protein_id="AAY52013.1"
                     /db_xref="GI:66731647"
                     /translation="MKKWGFLLLFLLCLGFAFINKALFFQDKVEIQKYDQNHKDNIDN
                     IENIGTPLSIQKNEIVKEQIYQGNLLLINSKYPIRQESVKSDIVNLSKHNELINGYGL
                     LNTNIYLSKGIAQKFSEMINDAVKEGVSQFFINSGYRDFDEQSVLYQEMGADYALPAG
                     YSEHNSGLSLDVGSSLTKMERAPEGKWLKENAWKYGFILRYPKDKTDVTGIQYEPWHI
                     RYVGFPHSAIMKEKNFALEEYMDFLKEQKSITTTIDHQVYKIFYYPISQNTTIPVPAN
                     GQYEISGNNMDGVIVTVYSGKRD"
     gene            7169. .7648
                     /gene="vanZ"
                     /operon="glycopeptide resistance vanA"
```

```
     CDS             7169. .7648
                     /gene="vanZ"
                     /operon="glycopeptide resistance vanA"
                     /note="teicoplanin resistance protein"
                     /codon_start=1
                     /transl_table=11
                     /product="VanZ"
                     /protein_id="AAY52015.1"
                     /db_xref="GI:66731649"
                     /translation="MNGGSRLKNWVVRAFFASYMYALFKIIVLKFGPTDVEFLWVRLM
                     RNSTNPECIAARLHAGNLIPLKEISRASDSMSGHSLLNLLGNVGIFVPLGIFLGVLAK
                     SGKLTLAGSFWSSLGVSLVLECTQVLFSIGTFDVDDLILNSIGGSIGFVVYALCALG"
     CDS             8782. .>9519
                     /note="Orf3; similar to BtrU in Bacillus circulans"
                     /codon_start=1
                     /transl_table=11
                     /product="BtrU-like protein"
                     /protein_id="AAY52014.1"
                     /db_xref="GI:66731648"
                     /translation="MPYALGGPDPLDGISAYKADRPNPHWHFVTYGFSELYDKESDNT
                     EDSGYGFELTFRLTRKEEEEEPPAWALNLLQNMGRYVFNSGNVFRAGDYLDANGPICL
                     ESDTQLTALSFVNDPELAAIDTPNGRVQFLQMIGITGDELEAMQTWNTLGVLSTGLQY
                     MPYYITDLERASLLRISAVSEAVHTGMGTEGSNTGFLFVSHLAWEPGKKGWLSKTPST
                     LKLGAKHAEIIGKLLRGRIMKGNKLSTI"
ORIGIN

  Query Match           100.0%;  Score 27;  DB 1;  Length 9519;
  Best Local Similarity  100.0%;  Pred. No. 0.38;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db       4622 CCTATCCTGTTTTTGTTAAGCCGGCGC 4648


RESULT 33
DQ018710
LOCUS       DQ018710               9537 bp    DNA     linear   BCT 31-MAY-2005
DEFINITION  Paenibacillus thiaminolyticus strain PT-2B1 putative transposase
            and putative GNAT family acetyltransferase genes, complete cds; and
            glycopeptide resistance vanA operon, partial sequence.
ACCESSION   DQ018710
VERSION     DQ018710.1  GI:66731632
KEYWORDS    .
SOURCE      Paenibacillus thiaminolyticus
  ORGANISM  Paenibacillus thiaminolyticus
            Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
REFERENCE   1  (bases 1 to 9537)
  AUTHORS   Guardabassi,L., Perichon,B., Van Heijenoort,J., Blanot,D. and
            Courvalin,P.
  TITLE     Glycopeptide resistance van operons in Paenibacillus from soil
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 9537)
  AUTHORS   Guardabassi,L., Perichon,B., Van Heijenoort,J., Blanot,D. and
            Courvalin,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-APR-2005) Unite des Agents Antibacteriens, Institut
            Pasteur, 25 rue du Docteur Roux, Paris 75015, France
FEATURES             Location/Qualifiers
     source          1. .9537
                     /organism="Paenibacillus thiaminolyticus"
                     /mol_type="genomic DNA"
                     /strain="PT-2B1"
                     /isolation_source="soil"
                     /db_xref="taxon:49283"
     CDS             1. .1263
                     /note="Orf1; similar to putative transposase in
                     Lactococcus lactis"
                     /codon_start=1
                     /transl_table=11
                     /product="putative transposase"
                     /protein_id="AAY52000.1"
                     /db_xref="GI:66731633"
                     /translation="MKTTLRPSKIKEILSNNIKSMAAIPDDYVRRPGHDFSRNRKLTF
                     ETMLQMLIGMGGNSLCKELYEWFSFSKDTASVSAFVQQREKILPSAIETLFHRFVASC
                     DESVLFNGYRLFAVDGTDLRLPTNPNDSESYMKNESNTKGYNLVHIDAMYDLMRHVYV
                     DASVQPKKGMNEHKALVSMVDRSNYSGKVIVIADRGYESFNNIAHFQEKSWNYIIRSK
                     ESYGIISKLAVPDQAEFDIQVTLSLTRRQTKQTLSLLKKDPVRYRWIQPHTTFDYLYP
                     KDDRLYDLCFRVVRFAISDVSYETVFTNLDSGNFPPDTIKELYNRRWGIETSFRELKY
                     AVGLVNLHSKKPSSMLQEVFSRFILYNFSALIAHQAQIPNEATKRINFSAAMLICRQY
                     FRDKLSEDSLLDLIAKHLSLIRKGRKFP"
     CDS             2120. .2524
                     /note="Orf2; similar to GNAT acetyltransferase in Bacillus
                     cereus"
                     /codon_start=1
                     /transl_table=11
                     /product="putative GNAT family acetyltransferase"
                     /protein_id="AAY52001.1"
                     /db_xref="GI:66731634"
                     /translation="MTTPLTYTVFLEEKKSSSVQQDNRWGLFVNDKLIGIVSYYWEHQ
                     ASNWLEAGLPIYNYDFWNGGYGTLFFKAWIDHLFKSLPLVRVGFTTWSGNQRMMRLGE
                     KLGMKLEGRLRKCRLVNGKYYDSIRMGILREE"
     operon          3048. .>9537
                     /operon="glycopeptide resistance vanA"
     gene            3048. .3743
                     /gene="vanR"
                     /operon="glycopeptide resistance vanA"
     CDS             3048. .3743
                     /gene="vanR"
                     /operon="glycopeptide resistance vanA"
                     /note="response regulator"
                     /codon_start=1
                     /transl_table=11
                     /product="VanR"
                     /protein_id="AAY52002.1"
                     /db_xref="GI:66731635"
                     /translation="MSDKILVVDDEHEIADLVELYLKNENYTVFKYYTAKEALECIDK
                     TDLDLAILDIMLPGASGLAICQKIRDKHTYPIIMLTAKDTEVDKITGLTIGADDYITK
                     SFRPLELIARVKAQLRRYKKYSGVAEQNENVIVHSGLVININTHECFLNEKQLSLTPT
                     EFSILRILCENKGNVVSSEQLFHEIWGDEYFSKSNNTITVHIRHLREKMNDTIDNPKY
                     IKTVWGVGYKIEK"
     gene            3721. .4881
                     /gene="vanS"
                     /operon="glycopeptide resistance vanA"
     CDS             3721. .4881
                     /gene="vanS"
                     /operon="glycopeptide resistance vanA"
                     /note="sensor histidine kinase"
                     /codon_start=1
                     /transl_table=11
                     /product="VanS"
                     /protein_id="AAY52003.1"
                     /db_xref="GI:66731636"
                     /translation="MAIKLKNKNKKTDYSKLKRKLYQYIVVIVMAAVVFVLFLRLFIK
                     GTLGEWIVRFLENSYHLERQDAMKIYQYTIRNNIEIFIYVAIAISILILCRVMLSKFA
                     KYFDEINTGIDILIQNEDKQIELSAEMEFMEQKLNTLKRTLEKREQDAKLAEQRKNDV
                     VMYLAHDIKTPLTSVIGYLSLLDEAPDMPVEQKAKYVHITLDKAYRLEQLIDEFFEIT
                     RYNLQTITLTKKHIDLYYMLVQMTDEFYPQLAANGKQAVIHASEDLTVSGDPDKLARV
                     FNNILKNAAAYSEDNSVIDITAGLSGDVVSIVFKNAGSIPKDKLAAIFEKFYRLDDAR
                     SSDTGGAGLGLAIAKEIIVQHGGQIYAESNDNYTTFTVELPALPDLVDKRSS"
     gene            5109. .6077
                     /gene="vanH"
                     /operon="glycopeptide resistance vanA"
     CDS             5109. .6077
                     /gene="vanH"
                     /operon="glycopeptide resistance vanA"
                     /note="dehydrogenase"
                     /codon_start=1
                     /transl_table=11
                     /product="VanH"
                     /protein_id="AAY52004.1"
                     /db_xref="GI:66731637"
                     /translation="MKNIGITVYGCEQDEADAFRALSPRFGIMPTIINAAVSEANAIS
                     APCNQCISVGHKSEVSASILLALKRAGVKYISTRSIGCNHIDTTAAKRMGIAVGNVAY
                     SPDSVADYTMMLMLMAVRNAKSIVRSVEKHDFRLDSVRGKVLRDMTVGVVGTGHIGKA
                     VIERLRGFGCHVLAYDRSQKIEANYVPFDALLQNSDIVTLHVPLNADTRHIIGHEQIK
```

```
                RMKQGAPIINTGRGPLVDTDALVKALENGKLGGAALDVLEGEEEFFYSDCSQKPIDNQ
                FLLKLQRMPNVIITPHTAYYTEQALRDTVEKTIKNCLDFERSQEHE"
     gene       6070. .7101
                /gene="vanA"
                /operon="glycopeptide resistance vanA"
     CDS        6070. .7101
                /gene="vanA"
                /operon="glycopeptide resistance vanA"
                /note="D-Ala:D-Lac ligase"
                /codon_start=1
                /transl_table=11
                /product="VanA"
                /protein_id="AAY52005.1"
                /db_xref="GI:66731638"
                /translation="MNRVKVAILFGGCSEEHDVSVKSAREIAANIDNEKYEPLYIGIT
                KPGVWKMCEKPCAEWENSNCYSAVLSPDKKMHGLLVKKNHEYEIHHVDVAFSVLHGKS
                GEDGSIQGLFELSGIPYVGCDIQSSAICMDKSLTYTIAKNAGIATPDFWVINKDDKPA
                IDAFTYPVFVKPARSGSSYGVKKVNGADELDAAIESARQYDSKILIEQAVLGCEVGCA
                VLGNSSELIVGEVDQIRLQHGIFRIHQEAEPEKGSENAVITIPADLSVEVRGRIQETA
                KKIYKALGCRGLSRVDMFLQDNGSIVLNEVNTLPGFTSYSRYPRMMVAAGITLPELID
                RLIVLALKG"
     gene       7107. .7715
                /gene="vanX"
                /operon="glycopeptide resistance vanA"
     CDS        7107. .7715
                /gene="vanX"
                /operon="glycopeptide resistance vanA"
                /note="D,D-dipeptidase"
                /codon_start=1
                /transl_table=11
                /product="VanX"
                /protein_id="AAY52006.1"
                /db_xref="GI:66731639"
                /translation="MKIGFTFLDEILHGVRWDAKYATWDNFTGKPVDGYEVNRIVGTY
                ELADALLKVKELAATQGYGLLLWDGYRPQRAVNCFLQWAAQPEDDLTKERYYPNIDRT
                EMVSKGYVASKSSHSRGSAIDLTLYRLDTGELVPMGSGFDFMDERSHHAAKGISGNEA
                QNRRRLRSIMEDSGFEAYSFEWWHYVLRNEPYPNSYFDFPVK"
     gene       8162. .9046
                /gene="vanY"
                /operon="glycopeptide resistance vanA"
     CDS        8162. .9046
                /gene="vanY"
                /operon="glycopeptide resistance vanA"
                /note="D,D-carboxypeptidase"
                /codon_start=1
                /transl_table=11
                /product="VanY"
                /protein_id="AAY52007.1"
                /db_xref="GI:66731640"
                /translation="MKKWGFLLLLCLGFVFINKALFFQEKVEIQNYDQNPKDHLDNRG
                TSESTQTKTITNEQIYQGNLLLFNSKYPVRQESVKSDIVNLSKHNELINGYGLLDTNI
                YMSKGIAQKFSEMVNDAVKEGVSHFIINSGYRDFDEQSVLYQEMGADYALPAGYSEHN
                SGLSLDVGSSLTKMERAPEGKWLKENAWKYGFILRYPKDKTDVTGIQYEPWHIRYVGF
                PHSAIMKEKNFALEEYMDFLKEQKSITTTIDHQVYKIFYYPISQNTTIHVPANGQYEI
                SGNNMDGVIVTVYSGKRD"
     gene       9108. .>9537
                /gene="vanZ"
                /operon="glycopeptide resistance vanA"
     CDS        9108. .>9537
                /gene="vanZ"
                /operon="glycopeptide resistance vanA"
                /note="teicoplanin resistance protein"
                /codon_start=1
                /transl_table=11
                /product="VanZ"
                /protein_id="AAY52008.1"
                /db_xref="GI:66731641"
                /translation="MGCSGFFSSYMYALFKIIVLKFGPTVVEFLWVRLMRNSTNPECI
                AARLHAGNLIPLKEISRASDSMSGHSLLNLFGNVGIFVPLGIPLGVLAKSGKLTLAGS
                SLVLECTQVLFSIGKFDVDDLILNSTGGSIGFVVYALCARL"
ORIGIN

  Query Match          100.0%;  Score 27;  DB 1;  Length 9537;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db       6563 CCTATCCTGTTTTTGTTAAGCCGGCGC 6589


RESULT 34
TRNVAN
LOCUS       TRNVAN                 10851 bp    DNA     linear   BCT 20-JUN-2002
DEFINITION  Enterococcus faecium transposon Tn1546 transposase, resolvase, vanR
            (vanR), vanS (vanS), vanH (vanH), vanA (vanA), vanX (vanX), vanY
            (vanY), and teicoplanin resistance protein (vanZ) genes, complete
            cds.
ACCESSION   M97297
VERSION     M97297.1  GI:155036
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1  (bases 1 to 10851)
  AUTHORS   Arthur,M., Molinas,C., Depardieu,F. and Courvalin,P.
  TITLE     Characterization of Tn1546, a Tn3-related transposon conferring
            glycopeptide resistance by synthesis of depsipeptide peptidoglycan
            precursors in Enterococcus faecium BM4147
  JOURNAL   J. Bacteriol. 175 (1), 117-127 (1993)
   PUBMED   8380148
REFERENCE   2  (bases 1 to 10851)
  AUTHORS   Arthur,M., Depardieu,F., Molinas,C., Reynolds,P. and Courvalin,P.
  TITLE     The vanZ gene of Tn1546 from Enterococcus faecium BM4147 confers
            resistance to teicoplanin
  JOURNAL   Gene 154 (1), 87-92 (1995)
   PUBMED   7867956
FEATURES             Location/Qualifiers
     source          1. .10851
                     /organism="Enterococcus faecium"
                     /mol_type="genomic DNA"
                     /specimen_voucher="BM4147"
                     /db_xref="taxon:1352"
                     /tissue_lib="BM 4147"
     repeat_region   1. .10851
                     /transposon="Tn1546"
     repeat_region   1. .38
                     /rpt_type=inverted
                     /transposon="Tn1546"
     CDS             complement(75. .3041)
                     /codon_start=1
                     /transl_table=11
                     /product="transposase"
                     /protein_id="AAA65951.1"
                     /db_xref="GI:155037"
                     /translation="MKIARGRELLTPEQRQAFMQIPEDEWILGTYFTFSKRDLEIVNK
                     RRREENRLGFAVQLAVLRYPGWPYTHIKSIPDSVIQYISKQIGVSPSSLDHYPQRENT
                     LWDHLKEIRSEYDFVTFTLSEYRMTFKYLHQLALENGDAIHLLHECIDFLRKNKIILP
                     AITTLERMVWEARAMAEKKLFNTVSKSLTNEQKEKLEGIITSQHPSESNKTILGWLKE
                     PPGHPSPETFLKIIERLEYIRGMDLETVQISHLHRNRLLQLSRLGSRYEPYAFRDFQE
                     NKRYSILTIYLLQLTQELTDKAFEIHDRQILSLLSKGRKAQEEIQKQNGKKLNEKVIH
                     FTNIGQALIKAREEKLDVFKVLESVIEWNTFVSSVEEAQELARPADYDYLDLLQKRFY
                     SLRKYTPTLLRVLEFHSTKANEPLLQAVEIIRGMNESGKRKVPDDSPVDFISKRWKRH
                     LYEDDGTTINRHYYEMAVLTELREHVRAGDVSIVGSRQYRDFEEYLFSEDTWNQSKGN
                     TRLSVSLSFEDYITERTSSFNERLKWLAANSNKLDGVSLEKGKLSLARLEKDVPEEAK
                     KFSASLYQMLPRIKLTDLLMDVAHITGFHEQFTHASNNRKPDKEETIIIMAALLGMGM
                     NIGLSKMAEATPGLTYKQLANVSQWRMYEDAMNKAQAILVNFHHKLQLPFYWGDGTTS
                     SSDGMRMQLGVSSLHADANPHYGTGKGATIYRFTSDQFSSYYTKIIHTNSRDAIHVLD
                     GLLHHETDLNIEEHYTDTAGYTDQIFGLTHLLGFKFAPRIRDLSDSKLFTIDKASEYP
                     KLEAILRGQINTKVIKENYEDVLRLAHSIREGTVSASLIMGKLGSYSRQNSLATALRE
                     MGRIEKTIFILNYISDESLRRKIQRGLNKGEAMNGLARAIFFGKQGELRERTIQHQLQ
                     RASALNIIINAISIWNTLHLTTAVEYKKRTGSFNEDLLHHMSPLGWEHINLLGEYHFN
                     SEKVVSLNSLRPLKLS"
     CDS             3187. .3762
                     /codon_start=1
```

```
                     /transl_table=11
                     /product="resolvase"
                     /protein_id="AAA65952.1"
                     /db_xref="GI:801883"
                     /translation="MRKIGYIRVSSTNQNPSRQFQQLNEIGMDIIYEEKVSGATKDRE
                     QLQKVLDDLQEDDIIYVTDLTRITRSTQDLFELIDNIRDKKASLKSLKDTWLDLSEDN
                     PYSQFLITVMAGVNQLERDLIRMRQREGIELAKKEGKFKGRLKKYHKNHAGMNYAVKL
                     YKEGNMTVNQICEITNVSRASLYRKLSEVNN"
     gene            3976. .4671
                     /gene="vanR"
     CDS             3976. .4671
                     /gene="vanR"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAA65953.1"
                     /db_xref="GI:155039"
                     /translation="MSDKILILVDDEHEIADLVELYLKNENYTVFKYYTAKEALECIDK
                     SEIDLAILDIMLPGTSGLTICQKIRDKHTYPIIMLTGKDTEVDKITGLTIGADDYITK
                     PFRPLELIARVKAQLRRYKKFSGVKEQNENVIVHSGLVINVNTHECYLNEKQLSLTPT
                     EFSILRILCENKGNVVSSELLFHEIWGDEYFSKSNNTITVHIRHLREKMNDTIDNPKY
                     IKTVWGVGYKIEK"
     gene            4649. .5803
                     /gene="vanS"
     CDS             4649. .5803
                     /gene="vanS"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAA65954.1"
                     /db_xref="GI:801884"
                     /translation="MVIKLKNKKNDYSKLERKLYMYIVAIVVVAIVFVLYIRSMIRGK
                     LGDWILSILENKYDLNHLDAMKLYQYSIRNNIDIFIYVAIVISILILCRVMLSKFAKY
                     FDEINTGIDVLIQNEDKQIELSAEMDVMEQKLNTLKRTLEKREQDAKLAEQRKNDVVM
                     YLAHDIKTPLTSIIGYLSLLDEAPDMPVDQKAKYVHITLDKAYRLEQLIDEFFEITRY
                     NLQTITLTKTHIDLYYMLVQMTDEFYPQLSAHGKQAVIHAPEDLTVSGDPDKLARVFN
                     NILKNAAAYSEDNSIIDITAGLSGDVVSIEFKNTGSIPKDKLAAIFEKFYRLDNARSS
                     DTGGAGLGLAIAKEIIVQHGGQIYAESNDNYTTFRVELPAMPDLVDKRRS"
     gene            6018. .6986
                     /gene="vanH"
     CDS             6018. .6986
                     /gene="vanH"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAA65955.1"
                     /db_xref="GI:155041"
                     /translation="MNNIGITVYGCEQDEADAFHALSPRFGVMATIINANVSESNAKS
                     APFNQCISVGHKSEISASILLALKRAGVKYISTRSIGCNHIDTTAAKRMGITVDNVAY
                     SPDSVADYTMMLILMAVRNVKSIVRSVEKHDFRLDSDRGKVLSDMTVGVVGTGQIGKA
                     VIERLRGFGCKVLAYSRSRSIEVNYVPFDELLQNSDIVTLHVPLNTDTHYIISHEQIQ
                     RMKQGAFLINTGRGPLVDTYELVKALENGKLGGAALDVLEGEEEFFYSDCTQKPIDNQ
                     FLLKLQRMPNVIITPHTAYYTEQALRDTVEKTIKNCLDFERRQEHE"
     gene            6979. .8010
                     /gene="vanA"
     CDS             6979. .8010
                     /gene="vanA"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAA65956.1"
                     /db_xref="GI:155042"
                     /translation="MNRIKVAILFGGCSEEHDVSVKSAIEIAANINKEKYEPLYIGIT
                     KSGVWKMCEKPCAEWENDNCYSAVLSPDKKMHGLLVKKNHEYEINHVDVAFSALHGKS
                     GEDGSIQGLFELSGIPFVGCDIQSSAICMDKSLTYIVAKNAGIATPAFWVINKDDRPV
                     AATFTYPVFVKPARSGSSFGVKKVNSADELDYAIESARQYDSKILIEQAVSGCEVGCA
                     VLGNSAALVVGEVDQIRLQYGIFRIHQEVEPEKGSENAVITVPADLSAEERGRIQETA
                     KKIYKALGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMAAAGIALPELID
                     RLIVLALKG"
     gene            8016. .8624
                     /gene="vanX"
     CDS             8016. .8624
                     /gene="vanX"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAA65957.1"
                     /db_xref="GI:155043"
                     /translation="MEIGFTFLDEIVHGVRWDAKYATWDNFTGKPVDGYEVNRIVGTY
                     ELAESLLKAKELAATQGYGLLLWDGYRPKRAVNCFMQWAAQPENNLTKESYYPNIDRT
                     EMISKGYVASKSSHSRGSAIDLTLYRLDTGELVPMGSRFDFMDERSHHAANGISCNEA
                     QNRRRLRSIMENSGFEAYSLEWWHYVLRDEPYPNSYFDFPVK"
     gene            9052. .9963
                     /gene="vanY"
     CDS             9052. .9963
                     /gene="vanY"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAA65958.1"
                     /db_xref="GI:155044"
                     /translation="MKKLFFLLLLLFLIYLGYDYVNEALFSQEKVEFQNYDQNPKEHL
                     ENSGTSENTQEKTITEEQVYQGNLLLINSKYPVRQESVKSDIVNLSKHDELINGYGLL
                     DSNIYMSKEIAQKFSEMVNDAVKGGVSHFIINSGYRDFDEQSVLYQEMGAEYALPAGY
                     SEHNSGLSLDVGSSLTKMERAPEGKWIEENAWKYGFILRYPEDKTELTGIQYEPWHIR
                     YVGLPHSAIMKEKNFVLEEYMDYLKEEKTISVSVNGEKYEIFYYPVTKNTTIHVPTNL
                     RYEISGNNIDGVIVTVFPGSTHTNSRR"
     gene            10116. .10601
                     /gene="vanZ"
     CDS             10116. .10601
                     /gene="vanZ"
                     /codon_start=1
                     /transl_table=11
                     /product="teicoplanin resistance protein"
                     /protein_id="AAA65959.1"
                     /db_xref="GI:801885"
                     /translation="MGKILSRGLLALYLVTLIWLVLFKLQYNILSVFNYHQRSLNLTP
                     FTATGNFREMIDNVIIFIPFGLLLNVNFKEIGFLPKFAFVLVLSLTFEIIQFIFAIGA
                     TDITDVITNTVGGFLGLKLYGLSNKHMNQKKLDRVIIFVGILLLVLLLVYRTHLRINY
                     V"
     repeat_region   10814. .10851
                     /rpt_type=inverted
                     /transposon="Tn1546"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 1;  Length 10851;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db       7472 CCTATCCTGTTTTTGTTAAGCCGGCGC 7498


RESULT 35
AR035513
LOCUS       AR035513               10851 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 16 from patent US 5871910.
ACCESSION   AR035513
VERSION     AR035513.1  GI:5952181
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10851)
  AUTHORS   Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
  TITLE     Probes for the detection of nucleotide sequences implicated in the
            expression of resistance to glycopeptides, in particular in
            gram-positive bacteria
  JOURNAL   Patent: US 5871910-A 16 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .10851
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 10851;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
```

```
Db       7472 CCTATCCTGTTTTTGTTAAGCCGGCGC 7498


RESULT 36
BD181854
LOCUS       BD181854               10851 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Polypeptides implicated in the expression of resistance to
            glycopeptides, in particular in gram-positive bacteria, nucleotide
            sequence cod ing for these polypeptides and use for diagnosis.
ACCESSION   BD181854
VERSION     BD181854.1  GI:30792772
KEYWORDS    JP 2002320494-A/10.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10851)
  AUTHORS   Arthur,M., DuktaMmalen,S., Molinas,C. and Courvalin,P.
  TITLE     Polypeptides implicated in the expression of resistance to
            glycopeptides, in particular in gram-positive bacteria, nucleotide
            sequence cod ing for these polypeptides and use for diagnosis
  JOURNAL   Patent: JP 2002320494-A 10 05-NOV-2002;
            INSTITUT PASTEUR
COMMENT     OS   Bacteria
            PN   JP 2002320494-A/10
            PD   05-NOV-2002
            PF   21-FEB-2002 JP 2002045484
            PR   31-OCT-1990 FR     90/13579
            PI   MICHEL ARTHUR,SYLVIE DUKTA-MALEN,CATHERINE MOLINAS,PATRICE  PI
              COURVALIN
            PC   C12N15/09,C07K14/315,C07K16/12,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12Q1/04,C12Q1/68,G01N33/53,G01N33/566,G01N33/569//C12P21/08,
            PC   (C12Q1/04,C12R1:01),(C12Q1/68,C12R1:01),C12N15/00,C12N5/00 CC
             Polypeptides implicated in the expression of resistance to  CC
                  glycopeptides,
            CC   in particular in gram-positive bacteria, nucleotide sequence
            CC            cod ing for
            CC   these polypeptides and use for diagnosis
            FH   Key             Location/Qualifiers
            FT   source          1. .10851
            FT                   /organism='Bacteria'.
FEATURES             Location/Qualifiers
     source          1. .10851
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 10851;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db       7472 CCTATCCTGTTTTTGTTAAGCCGGCGC 7498


RESULT 37
AX085648
LOCUS       AX085648               10851 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 1 from Patent WO0112803.
ACCESSION   AX085648
VERSION     AX085648.1  GI:13275634
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1
  AUTHORS   Inouye,R.T., Torres-Viera,C., Moellering,R., Gold,H. and
            Eliopoulos,G.M.
  TITLE     Methods and compositions for restoring antibiotic susceptibility in
            glycopeptide-resistant Enterococcus
  JOURNAL   Patent: WO 0112803-A 1 22-FEB-2001;
            Beth Israel Deaconess Medical Center, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10851
                     /organism="Enterococcus faecium"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1352"
ORIGIN

  Query Match             100.0%;  Score 27;  DB 6;  Length 10851;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||||||
Db       7472 CCTATCCTGTTTTTGTTAAGCCGGCGC 7498


RESULT 38
AF516335
LOCUS       AF516335               17510 bp    DNA     linear   BCT 28-AUG-2002
DEFINITION  Enterococcus faecium plasmid pUW786 multiple antibiotic resistance
            gene cluster, complete sequence.
ACCESSION   AF516335
VERSION     AF516335.1  GI:21886737
KEYWORDS    .
SOURCE      Enterococcus faecium
  ORGANISM  Enterococcus faecium
            Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
            Enterococcus.
REFERENCE   1  (bases 1 to 17510)
  AUTHORS   Werner,G., Klare,I. and Witte,W.
  TITLE     Multi-resistance gene cluster on a plasmid in a clinical isolate of
            Enterococcus faecium
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 17510)
  AUTHORS   Werner,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAY-2002) Wernigerode Branch, Robert Koch Institute,
            Burgstr. 37, Wernigerode 38855, Germany
FEATURES             Location/Qualifiers
     source          1. .17510
                     /organism="Enterococcus faecium"
                     /mol_type="genomic DNA"
                     /isolate="UW786"
                     /db_xref="taxon:1352"
                     /plasmid="pUW786"
     CDS             <1. .532
                     /codon_start=2
                     /transl_table=11
                     /product="putative resolvase"
                     /protein_id="AAM77881.1"
                     /db_xref="GI:21886738"
                     /translation="PSRQFQQLNEIGMDIIYEEKVSGATKDREQLQKVLDDLQEDDII
                     YVTDLTRITRSTQDLFELIDNIRDKKASLKSLKDTWLDLSEDNPYSQFLITVMAGVNQ
                     LERDLIRMRQREGIELAKKEGKFKGRLKKYHKNHAGMNYAVKLYKEGNMTVNQICEIT
                     NVSRASLYRKLSEVNN"
     repeat_region   <1. .532
                     /transposon="Tn1546"
     gene            746. .1441
                     /gene="vanR"
     CDS             746. .1441
                     /gene="vanR"
                     /note="regulator of two-component regulatory system"
                     /codon_start=1
                     /transl_table=11
                     /product="cytoplasmic regulator"
                     /protein_id="AAM77882.1"
                     /db_xref="GI:21886739"
                     /translation="MSDKILIVDDEHEIADLVELYLKNENYTVFKYYTAKEALECIDK
                     SEIDLAILDIMLPGTSGLTICQKIRDKHTYPIIMLTGKDTEVDKITGLTIGADDYITK
                     PFRPLELIARVKAQLRRYKKFSGVKEQNENVIVHSGLVINVNTHECYLNEKQLSLTPT
                     EFSILRILCENKGNVVSSELLFHEIWGDEYFSKSNNTITVHIRHLREKMNDTIDNPKY
```

```
                IKTVWGVGYKIEK"
gene            1419. .1463
                /gene="vanS"
                /allele="vanS'"
CDS             1419. .1463
                /gene="vanS"
                /allele="vanS'"
                /codon_start=1
                /transl_table=11
                /product="truncated protein kinase"
                /protein_id="AAM77883.1"
                /db_xref="GI:21886740"
                /translation="MVIKLKNKKTTIPN"
gene            2787. .3755
                /gene="vanH"
CDS             2787. .3755
                /gene="vanH"
                /codon_start=1
                /transl_table=11
                /product="pyruvate dehydrogenase"
                /protein_id="AAM77884.1"
                /db_xref="GI:21886741"
                /translation="MNNIGITVYGCEQDEADAFHALSPRFGVMATIINANVSESNAKS
                APFNQCISVGHKSEISASILLALKRAGVKYISTRSIGCNHIDTTAAKRMGITVDNVAY
                SPDSVADYTMMLILMAVRNVKSIVRSVEKHDFRLDSDRGKVLSDMTVGVVGTGQIGKA
                VIERLRGFGCKVLAYSRSRSIEVNYVPFDELLQNSDIVTLHVPLNTDTHYIISHEQIQ
                RMKQGAFLINTGRGPLVDTYELVKALENGKLGGAALDVLEGEEEFFYSDCTQKPIDNQ
                FLLKLQRMPNVIITPHTAYYTEQALRDTVEKTIKNCLDFERRQEHE"
gene            3748. .4779
                /gene="vanA"
CDS             3748. .4779
                /gene="vanA"
                /codon_start=1
                /transl_table=11
                /product="D-Ala-D-Lac ligase"
                /protein_id="AAM77885.1"
                /db_xref="GI:21886742"
                /translation="MNRIKVAILFGGCSEEHDVSVKSAIEIAANINKEKYEPLYIGIT
                KSGVWKMCEKPCAEWENDNCYSAVLSPDKKMHGLLVKKNHEYEINHVDVAFSALHGKS
                GEDGSIQGLFELSGIPFVGCDIQSSAICMDKSLTYIVAKNAGIATPAFWVINKDDRPV
                AATFTYPVFVKPARSGSSFGVKKVNSADELDYAIESARQYDSKILIIEQAVSGCEVGCA
                VLGNSAALVVGEVDQIRLQYGIFRIHQEVEPEKGSENAVITVPADLSAEERGRIQETA
                KKIYKALGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMAAAGIALPELID
                RLIVLALKG"
gene            4785. .5393
                /gene="vanX"
CDS             4785. .5393
                /gene="vanX"
                /codon_start=1
                /transl_table=11
                /product="D-Ala-D-Ala dipeptidase"
                /protein_id="AAM77886.1"
                /db_xref="GI:21886743"
                /translation="MEIGFTFLDEIVHGVRWDAKYATWDNFTGKPVDGYEVNRIVGTY
                ELAESLLKAKELAATQGYGLLLWDGYRPNRAVNCFMQWAAQPENNLTKESYYPNIDRT
                EMISKGYVASKSSHSRGSAIDLTLYRLDTGELVPMGSRFDFMDERSHHAANGISCNEA
                QNRRRLRSIMENSGFEAYSLEWWHYVLRDEPYPNSYFDFPVK"
gene            5821. .6366
                /gene="vanY"
                /allele="vanY'"
CDS             5821. .6366
                /gene="vanY"
                /allele="vanY'"
                /codon_start=1
                /transl_table=11
                /product="truncated carboxypeptidase"
                /protein_id="AAM77887.1"
                /db_xref="GI:21886744"
                /translation="MKKLFFLLLLLFLIYLGYDYVNEALFSQEKVEFQNYDQNPKEHL
                ENSGTSENTQEKTITEEQVYQGNLLLINSKYPVRQESVKSDIVNLSKHDELINGYGLL
                DSNIYMSKEIAQKFSEMVNDAVKGGVSHFIINSGYRDFDEQSVLYQEMGAEYALPAGY
                SEHNSGLSLDVGFCCKVLNKE"
repeat_region   complement(6335. .7143)
                /insertion_seq="IS1216V"
repeat_region   complement(6335. .6352)
                /note="IR"
                /rpt_type=inverted
CDS             complement(6389. .7075)
                /codon_start=1
                /transl_table=11
                /product="transposase"
                /protein_id="AAM77888.1"
                /db_xref="GI:21886745"
                /translation="MTMNHFKGKQFQQDVIIVAVGYYLRYNLSYREVQEILYDRGINV
                SHTTIYRWVQEYGKLLYQIWKKKNKKSFYSWKMDETYIKIKGKWHYLYRAIDADGLTL
                DIWLRKKRDTQAAYAFLKRLVKQFDEPKVVVTDKAPSITSAFKKLKEYGFYQGTEHRT
                IKYLNNLIEQDHRPVKRRNKFYRSLRTASTTIKGMEAIRGLYKKTRKEGTLFGFSVCT
                EIKVLLGIPA"
repeat_region   complement(7126. .7143)
                /note="IR"
                /rpt_type=inverted
CDS             7537. .7734
                /codon_start=1
                /transl_table=11
                /product="unknown"
                /protein_id="AAM77889.1"
                /db_xref="GI:21886746"
                /translation="MGDKTVRVRADLHHIIKIETAKNGGNVKEVMEIRLRSKLKSVLI
                VQYLKILCIIGIEVKLDAKNL"
CDS             7755. .7838
                /codon_start=1
                /transl_table=11
                /product="ermB methylase leader peptide"
                /protein_id="AAM77890.1"
                /db_xref="GI:21886747"
                /translation="MLVFQMRNVDKTSTVLKQTKNSDYTDK"
gene            7963. .8700
                /gene="ermB"
CDS             7963. .8700
                /gene="ermB"
                /codon_start=1
                /transl_table=11
                /product="ermB methylase"
                /protein_id="AAM77891.1"
                /db_xref="GI:21886748"
                /translation="MNKNIKYSQNFLTSEKVLNQIIKQLNLKETDTVYEIGTGKGHLT
                TKLAKISKQVTSIELDSHLFNLSSEKLKLNIRVTLIHQDILQFQFPNKQRYKIVGSIP
                YHLSTQIIKKVVFESHASDIYLIVEEGFYKRTLDIHRTLGLLLHTQVSIQQLLKLPAE
                CFHPKPKVNSVLIKLTRHTTDVPDKYWKLYTYFVSKWVNREYRQLFTKNQFHQAMKHA
                KVNNLSTVTYEQVLSIFNSYLLFNGRK"
repeat_region   9136. .>17510
                /transposon="Tn5405-like"
repeat_region   9136. .9168
                /note="IS1182 IR-R"
                /rpt_type=inverted
CDS             complement(join(9287. .9592,11012. .12001))
                /note="coding region disrupted by insertion sequence"
                /codon_start=1
                /transl_table=11
                /product="putative transposase"
                /protein_id="AAM77892.1"
                /db_xref="GI:21886749"
                /translation="MNDSIKKMLRITEKDLMITEVSYETLQKKKTLVVDAVLSPTPRA
                CRSCGSTVVDGNGKAIIVKNGKKETIVRFEQYNHMPLVMRLKKQRYTCKNCRTHWTAQ
                SYFVQPRHSIANHVRYKIASLLTEKVSLSFIAKSCQVSLTTVIRTLKEFKSYLPKQSK
                KILPRVLMVDEFRSHASIEDKMSFICADGETGKLIDVLPTRKLPRLTSYFLGCTNPEE
                VEFLVTDMNAAYFQLTKRVLPNAKVVIDRFHIVKHMNQAFNELRIREMNELRKAGQKS
                QAEKLKKNWRFLLKNRANINHYEYKTWKSFRAPKYPFLTEAMMIDRLLEFSPPLKEAY
                PFFHELVEAFRDKDPDLFFSLLAELPETLDDSFREKLQNLLTYEEGITNAMIYPYSNG
                KIEAKNTHIKTMKRVSYGFKSFENMRIRIFLINQLINVR"
repeat_region   9594. .11009
                /insertion_seq="IS150-like"
repeat_region   9594. .9613
                /note="IR-R"
                /rpt_type=inverted
CDS             9857. .10183
```

```
                     /codon_start=1

  Query Match             100.0%;  Score 27;  DB 1;  Length 17510;
  Best Local Similarity   100.0%;  Pred. No. 0.34;
  Matches    27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db       4241 CCTATCCTGTTTTTGTTAAGCCGGCGC 4267


RESULT 39
AE017171
LOCUS       AE017171               57889 bp    DNA     circular BCT 01-AUG-2003
DEFINITION  Staphylococcus aureus plasmid pLW043, complete sequence.
ACCESSION   AE017171
VERSION     AE017171.1  GI:33390917
KEYWORDS    .
SOURCE      Staphylococcus aureus
  ORGANISM  Staphylococcus aureus
            Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE   1  (bases 1 to 57889)
  AUTHORS   Gill,S., Kolonay,J., Shetty,J., Tenover,F. and Weigel,L.
  TITLE     Sequence of the Michigan vancomycin-resistant Staphylococcus aureus
            plasmid
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 57889)
  AUTHORS   Gill,S., Kolonay,J., Shetty,J., Tenover,F. and Weigel,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUL-2003) The Institute for Genomic Research, 9712
            Medical Center Dr., Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .57889
                     /organism="Staphylococcus aureus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1280"
                     /plasmid="pLW043"
     gene            101. .1060
                     /gene="repA"
                     /locus_tag="VRA0001"
     CDS             101. .1060
                     /gene="repA"
                     /locus_tag="VRA0001"
                     /note="similar to GP:3676426, and GP:1041637; identified
                     by sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="replication initiator protein"
                     /protein_id="AAQ17124.1"
                     /db_xref="GI:33390918"
                     /translation="MSKQFFTVEENYKERFYQLPKVFFTNPNYKDLSNDAKIAYAILR
                     DRLQLSIKNNWIDTEGNIYFIYTVADLEVILNCGNKKITKIKKELENVDLLIQKRQGL
                     NKPNLLYLLKPAITKNDIYEIDKAENEVEALQDKEVSKGHVQKCQKDTSRNVKRTRLE
                     MSKGHTNDTDFIDTDFIDTESNDMNNMNDTNQHSNHSNHFSNIHDKESLKYIELQELP
                     ELIKSYINNFSYEEVKSIKSVILKAKKSFNNKYDTFYMLEDIDEELLLVLKRFKGYLV
                     KKQEKVANMEGYLMRSIIAELEEMHSTIMRRKNMENNPLSLFN"
     gene            1179. .1853
                     /locus_tag="VRA0002"
     CDS             1179. .1853
                     /locus_tag="VRA0002"
                     /note="similar to GP:13383313, and SP:P19380; identified
                     by sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="IS431mec transposase"
                     /protein_id="AAQ17125.1"
                     /db_xref="GI:33390919"
                     /translation="MNYFRYKQFNKDVITVAVGYYLRYALSYRDISEILRGRGVNVHH
                     STVYRWVQEYAPILYQIWKKKHKKAYYKWRIDETYIKIKGKWSYLYRAIDAEGHTLDI
                     WLRKQRDNHSAYAFIKRLIKQFGKPQKVITDQAPSTKVAMVKVIKAFKLKPDCHCTSK
                     YLNNLIEQDHRHIKVRKTRYQSINTAKNTLKGIECIYALYKKNRRSLQIYGFSPCHEI
                     SIMLAS"
     gene            complement(1885. .2307)
                     /locus_tag="VRA0003"
     CDS             complement(1885. .2307)
                     /locus_tag="VRA0003"
                     /note="similar to GP:4105402; identified by sequence
                     similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="conserved hypothetical protein"
                     /protein_id="AAQ17126.1"
                     /db_xref="GI:33390920"
                     /translation="MAKQIIVTDSTSDLSHEYLKQHNIHVIPLSLTIDGKSYTDQVDI
                     SSSEYIDHIENDADVKTSQPPIGRFIETYEQLAQDDVEIISIHLSSGLSGTYNTAVQA
                     SHMVDGNITVIDSKSISFGLGYQIKQIVELVLLQSKKI"
     gene            complement(2317. .2802)
                     /gene="dfrA"
                     /locus_tag="VRA0004"
     CDS             complement(2317. .2802)
                     /gene="dfrA"
                     /locus_tag="VRA0004"
                     /note="similar to GP:13383309, and SP:P11045; identified
                     by sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="trimethoprim resistant dihydrofolate reductase"
                     /protein_id="AAQ17127.1"
                     /db_xref="GI:33390921"
                     /translation="MTLSIIVAHDKQRVIGYQNQLPWHLPNDLKHIKQLTTGNTLVMA
                     RKTFNSIGKPLPNRRNVVLTNQASFHHEGVDVINSLDEIKELSGHVFIFGGQTLYEAM
                     IDQVDDMYITVIDGKFQGDTFFPPYTFENWEVESSVEGQLDEKNTIPHTFLHLVRRKG
                     K"
     gene            complement(2844. .3800)
                     /gene="thyA"
                     /locus_tag="VRA0005"
     CDS             complement(2844. .3800)
                     /gene="thyA"
                     /locus_tag="VRA0005"
                     /note="similar to SP:P13954, and SP:P00469; identified by
                     sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="thymidylate synthase"
                     /protein_id="AAQ17128.1"
                     /db_xref="GI:33390922"
                     /translation="MYNPFDEAYHGLCEEILEIGNRRDDRTHTGTISKFGHQLRFDLT
                     KGFPLLTTKKVSFKLVATELLWFIKGDTNIQYLLKYNNNIWNEWAFENYVQSDDYHGP
                     DMTDFGHRSQQDPEFNEQYKEEMKKFKERILNDDAFAKKYGNLGNVYGKQWRDWEDKN
                     GNHYDQLKSVIQQIKTNPNSRRHIVSAWNPTEIDSMALPPCHTMFQFYVQEGKLNCQL
                     YQRSADIFLGVPFNIASYALLTHLVAKECGLEVGEFIHTFGDAHIYSNHMDAIHTQLS
                     RDSYLPPQLKINTDKSIFDINYEDLELINYESHPAIKAPIAV"
     gene            3914. .4588
                     /locus_tag="VRA0006"
     CDS             3914. .4588
                     /locus_tag="VRA0006"
                     /note="similar to SP:P14506, and SP:P19380; identified by
                     sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="IS431mec transposase"
                     /protein_id="AAQ17129.1"
                     /db_xref="GI:33390923"
                     /translation="MNYFRYKQFNKDVITVAVGYYLRYALSYRDISEILRGRGVNVHH
                     STVYRWVQEYAPILYQIWKKKHKKAYYKWRIDETYIKIKGKWSYLYRAIDAEGHTLDI
                     WLRKQRDNHSAYAFIKRLIKQFGKPQKVITDQAPSTKVAMAKVIKAFKLKPDCHCTSK
                     YLNNLIEQDHRHIKVRKTRYQSINTAKNTLKGIECIYALYKKNRRSLQIYGFSPCHEI
                     SIMLAS"
     gene            complement(4697. .4885)
                     /gene="artA"
                     /locus_tag="VRA0007"
     CDS             complement(4697. .4885)
                     /gene="artA"
                     /locus_tag="VRA0007"
                     /note="similar to GP:21623785; identified by sequence
                     similarity; putative"
```

```
                     /codon_start=1
                     /transl_table=11
                     /product="regulator of transfer gene ArtA"
                     /protein_id="AAQ17130.1"
                     /db_xref="GI:33390924"
                     /translation="MNNNEENSVFFGKKKKVSLHLLVDPDMKDEIIKYAQEKDFDNVS
                     QAGREILKKGLEQIKSNK"
     gene            5057. .6031
                     /gene="traA"
                     /locus_tag="VRA0008"
     CDS             5057. .6031
                     /gene="traA"
                     /locus_tag="VRA0008"
                     /note="similar to GP:3676435, GB:X15505, GB:D45417,
                     SP:P15951, SP:P35030, and PID:37460; identified by
                     sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="TraA"
                     /protein_id="AAQ17131.1"
                     /db_xref="GI:33390925"
                     /translation="MDNITFRKRIEEYRKRSIEQKKYESKLNYQSRFGVKDDEVSTFN
                     IKGIATDKKENKLVMAEDREDKQKVLLYANKDNDMYYLNSGSTYKEAVQNTFGNETNY
                     EMVDDELFIYNSKNQALTNYDQLDEYHNRQKQLQYNTKLEQERKQRLTDTNKVSENAK
                     EDLALSLGLTATALKGNINISNVEKVTDNESMVTIENEINGKSEHLISDFKDSFIEKA
                     KEKLTVSPSMRLGFEEFKNASGQIAMGFTEFFGARYDESTLENDPKVVATEKGYSVSV
                     FDKDGNKKDLTSADTFEEAVKLSKEMKHDNSLSRSEIELNQELEKKKI"
     gene            6048. .6365
                     /gene="traB"
                     /locus_tag="VRA0009"
     CDS             6048. .6365
                     /gene="traB"
                     /locus_tag="VRA0009"
                     /note="similar to GP:3676436; identified by sequence
                     similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="TraB"
                     /protein_id="AAQ17132.1"
                     /db_xref="GI:33390926"
                     /translation="MIKKFSLTTVYVAFLSIVLSNITLGAENPGPKIEQGLQQVQTFL
                     TGLIVAVGICAGVWIVLKKLPGIDDPMVKNEMFRGVGMVLAGVAVGAALVWLVPWVYN
                     LFQ"
     gene            6425. .6832
                     /gene="traC"
                     /locus_tag="VRA0010"
     CDS             6425. .6832
                     /gene="traC"
                     /locus_tag="VRA0010"
                     /note="similar to GP:3676437; identified by sequence
                     similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="TraC"
                     /protein_id="AAQ17133.1"
                     /db_xref="GI:33390927"
                     /translation="MSVEQEVKDIMLDMLGEEKKVKENIIPRNVDASYKIFLNLNGKE
                     LAIVFVPFLLFLTIAFGVTFLMGLLNLITGFMVFIVGLIFGLTIYGLLTIRPISTKEN
                     IRMIDTIKQSQRFSRRQKVYFYKSKEGLGDDDV"
     gene            6819. .7502
                     /gene="traD"
                     /locus_tag="VRA0011"
     CDS             6819. .7502
                     /gene="traD"
                     /locus_tag="VRA0011"
                     /note="similar to GP:3676438, and GP:3676438; identified
                     by sequence similarity; putative"

  Query Match             100.0%;  Score 27;  DB 1;  Length 57889;
  Best Local Similarity   100.0%;  Pred. No. 0.29;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db      34792 CCTATCCTGTTTTTGTTAAGCCGGCGC 34818


RESULT 40
BCY15704
LOCUS       BCY15704               1054 bp    DNA     linear   BCT 18-APR-2005
DEFINITION  Bacillus circulans vanA gene.
ACCESSION   Y15704
VERSION     Y15704.1  GI:6448487
KEYWORDS    vanA gene.
SOURCE      Bacillus circulans
  ORGANISM  Bacillus circulans
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
REFERENCE   1
  AUTHORS   Ligozzi,M., Lo Cascio,G. and Fontana,R.
  TITLE     vanA gene cluster in a vancomycin-resistant clinical isolate of
            Bacillus circulans
  JOURNAL   Antimicrob. Agents Chemother. 42 (8), 2055-2059 (1998)
   PUBMED   9687406
REFERENCE   2  (bases 1 to 1054)
  AUTHORS   Ligozzi,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-NOV-1997) M. Ligozzi, Universita di Verona, Istituto
            di Microbiologia, Strada le Grazie 8, 37100 Verona, ITALY
FEATURES             Location/Qualifiers
     source.         1. .1054
                     /organism="Bacillus circulans"
                     /mol_type="genomic DNA"
                     /strain="VR0709"
                     /db_xref="taxon:1397"
     RBS             6. .13
     gene            23. .1054
                     /gene="vanA"
     CDS             23. .1054
                     /gene="vanA"
                     /codon_start=1
                     /transl_table=11
                     /product="vana protein"
                     /protein_id="CAB61227.1"
                     /db_xref="GI:6448488"
                     /db_xref="GOA:Q9RMA6"
                     /db_xref="InterPro:IPR000291"
                     /db_xref="InterPro:IPR005905"
                     /db_xref="InterPro:IPR011095"
                     /db_xref="InterPro:IPR011127"
                     /db_xref="InterPro:IPR011761"
                     /db_xref="UniProt/TrEMBL:Q9RMA6"
                     /translation="MNRIKVAILFGGCSEEHDVSVKSAIEIAANIDKEKYETLYIGIT
                     KSGVWKMCEKPCVEWENDNCCSAVLSPDKKMHGLLVKKNHEYEIDHVDVAFSVLHGKS
                     GEDGSIQGLFELSGIPFVGCDIQSSAICMDKSLTYIVAENAGIATPEFWVFNKDDKPM
                     ADTFTYPVFVKPARSGSSFGVKKVNGADELDAAIELAGQYDSKILIEQAVLGCEVGCA
                     VLGNSSAFVVGEVDQIRLQHGIFRIHQEAEPEKGSENAVITVPADLSAEERGRIQETA
                     KKIYNALGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMAAVGIAFPELID
                     RLIVLALKG"
ORIGIN

  Query Match             94.1%;  Score 25.4;  DB 1;  Length 1054;
  Best Local Similarity   96.3%;  Pred. No. 2.6;
  Matches   26;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||||||||||||||||||||||| ||||
Db        516 CCTATCCTGTTTTTGTTAAGCCTGCGC 542


Search completed: April  9, 2006, 07:14:32
Job time : 1052.14 secs
```

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 05:55:33 ; Search time 381.134 Seconds
(without alignments)
472.135 Million cell updates/sec

Title: US-10-661-094-1_COPY_870_896
Perfect score: 27
Sequence: 1 cctatcctgtttttgttaagccggcgc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27	100.0	27	14	ADY59929	Ady59929 Enterococ
2	27	100.0	1032	4	AAH02300	Aah02300 Enterococ
3	27	100.0	1032	4	AAF76039	Aaf76039 Enterococ
4	27	100.0	1218	4	AAH01064	Aah01064 Enterococ
5	27	100.0	1232	4	AAH01063	Aah01063 Enterococ
6	27	100.0	1237	4	AAH01061	Aah01061 Enterococ
7	27	100.0	1241	4	AAH01058	Aah01058 Enterococ
8	27	100.0	1249	4	AAH01059	Aah01059 Enterococ
9	27	100.0	1263	4	AAH01062	Aah01062 Enterococ
10	27	100.0	1265	4	AAH01065	Aah01065 Enterococ
11	27	100.0	1269	4	AAH01066	Aah01066 Enterococ
12	27	100.0	1272	4	AAH01060	Aah01060 Enterococ
13	27	100.0	1768	4	AAH01148	Aah01148 Enterococ
14	27	100.0	1768	12	ADO47257	Ado47257 E. faeciu
15	27	100.0	1768	14	ADY59927	Ady59927 Enterococ
16	27	100.0	2607	2	AAT28569	Aat28569 Bacterial
17	27	100.0	2607	4	ABA76994	Aba76994 Antibioti
18	27	100.0	3946	4	AAH01150	Aah01150 Enterococ
19	27	100.0	7227	2	AAQ25183	Aaq25183 E.faecium
20	27	100.0	10851	2	AAQ25178	Aaq25178 E.faecium
21	27	100.0	10851	4	AAF76019	Aaf76019 E. faeciu
22	20.8	77.0	1071	8	ACA22997	Aca22997 Prokaryot
23	20.8	77.0	110000	2	AAX20248_07	Continuation (8 of
c 24	20.6	76.3	555	12	ADO47266	Ado47266 Enterococ
c 25	20.6	76.3	556	12	ADO47264	Ado47264 Enterococ
c 26	20.6	76.3	556	12	ADO47262	Ado47262 E. faecal
c 27	20.6	76.3	556	12	ADO47263	Ado47263 E. faecal
c 28	20.6	76.3	556	12	ADO47261	Ado47261 E. faecal
c 29	20.6	76.3	556	12	ADO47265	Ado47265 E. faecal
c 30	20.6	76.3	556	12	ADO47260	Ado47260 E. faecal
c 31	20.6	76.3	556	12	ADO47259	Ado47259 E. faecal
32	20.6	76.3	589	2	AAQ69230	Aaq69230 Enterococ
33	20.6	76.3	630	14	ADY59941	Ady59941 Enterococ
34	20.6	76.3	783	14	ADY59942	Ady59942 Enterococ
35	20.6	76.3	801	4	AAH01126	Aah01126 Enterococ
c 36	20.6	76.3	801	14	ADY59937	Ady59937 Enterococ
c 37	20.6	76.3	801	14	ADY59940	Ady59940 Enterococ
c 38	20.6	76.3	801	14	ADY59943	Ady59943 Consensus
c 39	20.6	76.3	801	14	ADY59939	Ady59939 Enterococ
c 40	20.6	76.3	801	14	ADY59936	Ady59936 Enterococ
c 41	20.6	76.3	801	14	ADY59938	Ady59938 Enterococ
c 42	20.6	76.3	881	12	ADO47258	Ado47258 Enterococ
43	20.6	76.3	1029	2	AAV37115	Aav37115 Antibioti
44	20.6	76.3	1029	4	AAH02303	Aah02303 Enterococ
45	20.6	76.3	1029	4	AAH01720	Aah01720 Enterococ
46	20.6	76.3	1029	4	AAF76048	Aaf76048 Enterococ
47	20.6	76.3	1090	14	ADY59931	Ady59931 Enterococ
48	20.6	76.3	1128	10	ADC90583	Adc90583 E. faeciu
49	20.6	76.3	1141	2	AAQ69235	Aaq69235 Enterococ
50	20.6	76.3	7160	4	AAF76020	Aaf76020 E. faecal
51	20.6	76.3	7678	2	AAX12998	Aax12998 Enterococ
52	20.6	76.3	7678	6	ABS98793	Abs98793 Enterococ
53	19.8	73.3	594	3	AAA38150	Aaa38150 D alanine
54	19.8	73.3	1047	8	ACA48219	Aca48219 Prokaryot
55	19.6	72.6	1191	8	ACA52513	Aca52513 Prokaryot
56	19.6	72.6	21170	2	AAX20535	Aax20535 Polynucle
57	19	70.4	2000	11	ACL36388	Acl36388 Rice stre
58	18.6	68.9	1032	4	AAH01601	Aah01601 Enterococ
59	18.6	68.9	1032	4	AAF76056	Aaf76056 Enterococ
60	18.6	68.9	1280	14	AEB26980	Aeb26980 Pinus rad
61	18.6	68.9	5781	4	AAF76022	Aaf76022 E. faeciu
62	18.2	67.4	774	5	AAS81838	Aas81838 DNA encod
63	18.2	67.4	819	4	AAS52598	Aas52598 E. coli D
64	18.2	67.4	819	13	ADT48822	Adt48822 Bacterial
65	18.2	67.4	1473	13	ADT42360	Adt42360 Bacterial
c 66	18.2	67.4	95109	6	ABQ99654	Abq99654 Human mem
c 67	18	66.7	1206	8	ACA45223	Aca45223 Prokaryot
68	18	66.7	6378	12	ADQ21325	Adq21325 Human sof
69	18	66.7	6502	13	ACN43122	Acn43122 Human dia
70	18	66.7	6592	12	ADQ25197	Adq25197 Human sof
71	17.8	65.9	747	10	ADC81391	Adc81391 Carbonyl
72	17.8	65.9	753	10	ADC81379	Adc81379 Carbonyl
73	17.8	65.9	772	10	ADC81402	Adc81402 Carbonyl
74	17.8	65.9	1158	10	ADC81397	Adc81397 Carbonyl
c 75	17.8	65.9	1394	5	AAS90802	Aas90802 DNA encod
c 76	17.8	65.9	2013	13	ADU00970	Adu00970 DNA encod
c 77	17.8	65.9	2013	13	ADU15352	Adu15352 Novel hum
78	17.8	65.9	88208	14	ADZ13389	Adz13389 Human can
79	17.8	65.9	88445	13	ABD33536	Abd33536 Human can
80	17.8	65.9	121434	12	ADN30326	Adn30326 Human Not
81	17.8	65.9	121434	14	AEA08528	Aea08528 Human Not
82	17.6	65.2	251	12	ADQ06952	Adq06952 Soybean t
83	17.6	65.2	255	12	ADQ06944	Adq06944 Soybean t
84	17.6	65.2	263	12	ADQ06948	Adq06948 Soybean t
85	17.6	65.2	263	12	ADQ06946	Adq06946 Soybean t
86	17.6	65.2	268	12	ADQ06951	Adq06951 Soybean t
87	17.6	65.2	273	12	ADQ06945	Adq06945 Soybean t
c 88	17.6	65.2	277	5	ABV16923	Abv16923 Human pro
89	17.6	65.2	290	12	ADQ06950	Adq06950 Soybean t
c 90	17.6	65.2	430	5	ABV46718	Abv46718 Human pro
c 91	17.6	65.2	525	11	ACH96095	Ach96095 Klebsiell
92	17.6	65.2	943	13	ADX11876	Adx11876 Plant ful

93	17.6	65.2	1026	4	AAS53038	Aas53038 Enterococ
94	17.6	65.2	4948	2	AAT42134	Aat42134 I2C-1 gen
95	17.6	65.2	39982	8	AAD48290	Aad48290 Human enz
96	17.6	65.2	66685	4	AAS07380	Aas07380 Human gen
97	17.6	65.2	66686	6	ABS73149	Abs73149 Human CLA
98	17.4	64.4	318	10	ACF68191	Acf68191 Photorhab
c 99	17.4	64.4	486	4	AAH34587	Aah34587 Human col
c 100	17.4	64.4	747	3	AAZ54529	Aaz54529 Neisseria
c 101	17.4	64.4	754	12	ADO62241	Ado62241 Transcrip
c 102	17.4	64.4	1053	11	ABD12733	Abd12733 Pseudomon
c 103	17.4	64.4	1200	13	ADX60608	Adx60608 Plant ful
c 104	17.4	64.4	1262	12	ADO63288	Ado63288 Transcrip
c 105	17.4	64.4	1310	12	ADO62242	Ado62242 Transcrip
c 106	17.4	64.4	1353	13	ADX53082	Adx53082 Plant ful
107	17.4	64.4	1512	11	ABD12707	Abd12707 Pseudomon
c 108	17.4	64.4	1865	12	ADO62245	Ado62245 Transcrip
109	17.4	64.4	2334	11	ABD12689	Abd12689 Pseudomon
c 110	17.4	64.4	3274	2	AAV17622	Aav17622 Pisum sat
c 111	17.4	64.4	4081	2	AAV06585	Aav06585 Arabidops
c 112	17.4	64.4	23070	9	ADA02507	Ada02507 Mouse Wnt
c 113	17.4	64.4	23070	10	ADB72245	Adb72245 Mouse Wnt
c 114	17.4	64.4	23070	10	ADE95755	Ade95755 Mouse Wnt
c 115	17.4	64.4	23982	14	ADZ12503	Adz12503 Murine ca
116	17.4	64.4	73882	13	ADS73531	Ads73531 tcp gene
c 117	17.4	64.4	110000	10	ACF67367_09	Continuation (10 o
c 118	17.4	64.4	110000	10	ACF65384_3	Continuation (4 of
119	17.4	64.4	111836	13	ABD33102	Abd33102 Murine ca
120	17.4	64.4	256525	11	ACN44148	Acn44148 Mouse gen

ALIGNMENTS

RESULT 1
ADY59929
ID ADY59929 standard; DNA; 27 BP.
XX
AC ADY59929;
XX
DT 02-JUN-2005 (first entry)
XX
DE Enterococcus faecium vanA probe SEQ ID NO:3.
XX
KW DNA detection; antibiotic-resistance; vancomycin; vanA; probe; ss.
XX
OS Enterococcus faecium.
OS Synthetic.
XX
PN US2005058985-A1.
XX
PD 17-MAR-2005.
XX
PF 12-SEP-2003; 2003US-00661094.
XX
PR 12-SEP-2003; 2003US-00661094.
XX
PA (DODG/) DODGSON K J.
XX
PI Dodgson KJ;
XX
DR WPI; 2005-222218/23.
XX
PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX
PS Claim 34; SEQ ID NO 3; 33pp; English.
XX
CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents a
CC probe for Enterococcus faecium vanA, which is used in an example from the
CC present invention.
XX
SQ Sequence 27 BP; 3 A; 8 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 14; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27

RESULT 2
AAH02300
ID AAH02300 standard; DNA; 1032 BP.
XX
AC AAH02300;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecium nucleotide sequence SEQ ID NO:2293.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecium.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Disclosure; Page 1578; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic

CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1032 BP; 303 A; 197 C; 264 G; 268 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 494 CCTATCCTGTTTTTGTTAAGCCGGCGC 520

RESULT 3
AAF76039
ID AAF76039 standard; DNA; 1032 BP.
XX
AC AAF76039;
XX
DT 22-MAY-2001 (first entry)
XX
DE Enterococcus faecium vanA gene, SEQ ID NO:21.
XX
KW Vancomycin resistance reduction; antisense expression inhibition;
KW competitive inducer sequestration; vanH promoter; vanR gene product;
KW Enterococcus; Staphylococcus; Streptococcus; Gram-positive bacterium;
KW antibiotic susceptibility; ex vivo eradication; in vivo eradication;
KW glycopeptide resistance; VanA gene cluster; ds.
XX
OS Enterococcus faecium.
XX
PN WO200112803-A2.
XX
PD 22-FEB-2001.
XX
PF 11-AUG-2000; 2000WO-US022086.
XX
PR 17-AUG-1999; 99US-0149313P.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Inouye RT, Torres-Viera C, Moellering R, Gold H, Eliopoulos GM;
XX
DR WPI; 2001-211216/21.
XX
PT Reducing vancomycin-resistance in vancomycin-resistant organism by
PT introducing a antisense vancomycin-resistance molecule to inhibit
PT vancomycin-resistance gene expression, or by enhancing vanH promoter
PT expression.
XX
PS Example; Page 52; 59pp; English.
XX
CC The invention relates to methods of reducing vancomycin resistance in a
CC vancomycin-resistant organism. One method involves introducing a
CC vancomycin resistance gene antisense nucleic acid into the organism;
CC antisense oligonucleotides complementary to AAF76023-AAF76031 are
CC particularly preferred for this purpose. The second method involves
CC providing additional vanH promoter sequences which are not operatively
CC coupled to a vancomycin resistance gene, so that the phosphorylated vanR
CC gene product (which induces vanH promoter activity) is competitively
CC sequestered. Both methods are able to restore antibiotic susceptibility
CC in glycopeptide resistant enterococci. The methods of the invention are
CC useful for reducing vancomycin resistance in a vancomycin resistant
CC organism, particularly Enterococcus faecium and Enterococcus faecalis,
CC but also in other Gram-positive bacteria such as Staphylococcus sp. and
CC Streptococcus sp., to which Enterococcus faecium and Enterococcus
CC faecalis have the potential to transfer resistance determinants. The
CC antisense molecules are useful in the treatment of infection and
CC colonisation by vancomycin resistant enterococci and other clinically
CC significant pathogens, and may be used for the ex vivo eradication of
CC vancomycin-resistant enterococci from frequently colonised settings, such
CC as intensive care units, haemodialysis units, and chronic care facilities
CC ; for the in vivo clearance of vancomycin- resistant enterococci from
CC colonised gastrointestinal or genitourinary tracts of animals, including
CC humans; and in primary or adjuvant therapy for vancomycin-resistant
CC enterococcal infections. The gene based strategy targets key vancomycin
CC resistance determinants and results in restoration of vancomycin
CC susceptibility in previously glycopeptide- resistant enterococci.
CC Sequences AAF67036-AAF67042 represent genes of the Enterococcus faecium
CC VanA gene cluster
XX
SQ Sequence 1032 BP; 303 A; 197 C; 264 G; 268 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 494 CCTATCCTGTTTTTGTTAAGCCGGCGC 520

RESULT 4
AAH01064
ID AAH01064 standard; DNA; 1218 BP.
XX
AC AAH01064;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus gallinarum nucleotide sequence SEQ ID NO:1055.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus gallinarum.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX

DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 1001-1002; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1218 BP; 364 A; 226 C; 311 G; 317 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 568 CCTATCCTGTTTTTGTTAAGCCGGCGC 594

RESULT 5
AAH01063
ID AAH01063 standard; DNA; 1232 BP.
XX
AC AAH01063;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecalis nucleotide sequence SEQ ID NO:1054.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecalis.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 1001; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1232 BP; 367 A; 228 C; 313 G; 323 T; 0 U; 1 Other;

Query Match 100.0%; Score 27; DB 4; Length 1232;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 578 CCTATCCTGTTTTTGTTAAGCCGGCGC 604

RESULT 6
AAH01061
ID AAH01061 standard; DNA; 1237 BP.
XX
AC AAH01061;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecium nucleotide sequence SEQ ID NO:1052.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecium.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX

PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 999; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1237 BP; 366 A; 235 C; 314 G; 322 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1237;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 590 CCTATCCTGTTTTTGTTAAGCCGGCGC 616

RESULT 7
AAH01058
ID AAH01058 standard; DNA; 1241 BP.
XX
AC AAH01058;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecium nucleotide sequence SEQ ID NO:1049.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecium.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 997; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1241 BP; 371 A; 228 C; 317 G; 325 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1241;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 561 CCTATCCTGTTTTTGTTAAGCCGGCGC 587

RESULT 8
AAH01059
ID AAH01059 standard; DNA; 1249 BP.
XX
AC AAH01059;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus gallinarum nucleotide sequence SEQ ID NO:1050.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;

KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus gallinarum.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 998; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1249 BP; 373 A; 235 C; 316 G; 325 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1249;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 590 CCTATCCTGTTTTTGTTAAGCCGGCGC 616

RESULT 9
AAH01062
ID AAH01062 standard; DNA; 1263 BP.
XX
AC AAH01062;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecium nucleotide sequence SEQ ID NO:1053.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecium.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 1000; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1263 BP; 378 A; 234 C; 321 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1263;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 582 CCTATCCTGTTTTTGTTAAGCCGGCGC 608

RESULT 10
AAH01065
ID AAH01065 standard; DNA; 1265 BP.

XX
AC AAH01065;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecium nucleotide sequence SEQ ID NO:1056.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecium.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 1002; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1265 BP; 379 A; 237 C; 320 G; 329 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1265;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 592 CCTATCCTGTTTTTGTTAAGCCGGCGC 618

RESULT 11
AAH01066
ID AAH01066 standard; DNA; 1269 BP.
XX
AC AAH01066;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus flavescens nucleotide sequence SEQ ID NO:1057.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus flavescens.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 1003; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1269 BP; 380 A; 238 C; 321 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1269;
Best Local Similarity 100.0%; Pred. No. 0.031;

```
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db        590 CCTATCCTGTTTTTGTTAAGCCGGCGC 616


RESULT 12
AAH01060
ID   AAH01060 standard; DNA; 1272 BP.
XX
AC   AAH01060;
XX
DT   24-JUL-2001  (first entry)
XX
DE   Enterococcus faecium nucleotide sequence SEQ ID NO:1051.
XX
KW   Species specific; genus specific; family specific; probe; detection;
KW   identification; algal; archaeal; bacterial; fungal; parasitical;
KW   microorganism; diagnosis; translation elongation factor Tu; toxin;
KW   translation elongation factor G; RecA recombinase; resistance;
KW   catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW   primer; ds.
XX
OS   Enterococcus faecium.
XX
PN   WO200123604-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-CA001150.
XX
PR   28-SEP-1999;   99CA-02283458.
PR   19-MAY-2000; 2000CA-02307010.
XX
PA   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI   Bergeron MG,  Boissinot M,  Huletsky A,  Menard C,  Ouellette M;
PI   Picard FJ,  Roy PH;
XX
DR   WPI; 2001-245006/25.
XX
PT   Nucleic acid sequences are used to generate universal probes and primers
PT   which can be used to identify and detect the presence of algal, archaeal,
PT   bacterial, fungal and parasitical species in a test sample.
XX
PS   Claim 27; Page 998-999; 1580pp; English.
XX
CC   The present invention describes a method for generating a repertory of
CC   nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC   and/or primers are derived. The method comprises amplifying the nucleic
CC   acids of determined algal, archaeal, bacterial, fungal and parasitical
CC   species with a combination of defined primer pairs. The method can be
CC   used for producing probes and/or primers for detecting one or more
CC   related microorganisms e.g. algae, archaea, bacteria, fungi and
CC   parasites, for universal detection and for specific and ubiquitous
CC   detection and identification of an algal, archaeal, bacterial, fungal and
CC   parasitical species, genus, family and group. A nucleic acid (I) obtained
CC   using the method of the invention can be used for the universal detection
CC   of any bacterium, fungus or parasite in a sample and for the detection of
CC   at least one antimicrobial agent resistance gene or at least one toxin
CC   gene. hexA nucleic acids are used for the specific and ubiquitous
CC   detection and for identification of Streptococcus pneumoniae. (I) can be
CC   used to design a therapeutic agent which is effective against
CC   microorganisms. Microbial species or genus or family or phylum or group
CC   which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC   Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC   Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC   gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC   results than substrate specificity tests as results can be determined in
CC   an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC   represent nucleotide sequences and primers/probes which are given in the
CC   exemplification of the present invention
XX
SQ   Sequence 1272 BP; 379 A; 232 C; 325 G; 336 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 27;  DB 4;  Length 1272;
  Best Local Similarity   100.0%;  Pred. No. 0.031;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db        570 CCTATCCTGTTTTTGTTAAGCCGGCGC 596


RESULT 13
AAH01148
ID   AAH01148 standard; DNA; 1768 BP.
XX
AC   AAH01148;
XX
DT   24-JUL-2001  (first entry)
XX
DE   Enterococcus faecium nucleotide sequence SEQ ID NO:1139.
XX
KW   Species specific; genus specific; family specific; probe; detection;
KW   identification; algal; archaeal; bacterial; fungal; parasitical;
KW   microorganism; diagnosis; translation elongation factor Tu; toxin;
KW   translation elongation factor G; RecA recombinase; resistance;
KW   catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW   primer; ds.
XX
OS   Enterococcus faecium.
XX
PN   WO200123604-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-CA001150.
XX
PR   28-SEP-1999;   99CA-02283458.
PR   19-MAY-2000; 2000CA-02307010.
XX
PA   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI   Bergeron MG,  Boissinot M,  Huletsky A,  Menard C,  Ouellette M;
PI   Picard FJ,  Roy PH;
XX
DR   WPI; 2001-245006/25.
XX
PT   Nucleic acid sequences are used to generate universal probes and primers
PT   which can be used to identify and detect the presence of algal, archaeal,
PT   bacterial, fungal and parasitical species in a test sample.
XX
PS   Disclosure; Page 1033-1034; 1580pp; English.
XX
CC   The present invention describes a method for generating a repertory of
CC   nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC   and/or primers are derived. The method comprises amplifying the nucleic
CC   acids of determined algal, archaeal, bacterial, fungal and parasitical
CC   species with a combination of defined primer pairs. The method can be
CC   used for producing probes and/or primers for detecting one or more
CC   related microorganisms e.g. algae, archaea, bacteria, fungi and
CC   parasites, for universal detection and for specific and ubiquitous
CC   detection and identification of an algal, archaeal, bacterial, fungal and
CC   parasitical species, genus, family and group. A nucleic acid (I) obtained
CC   using the method of the invention can be used for the universal detection
CC   of any bacterium, fungus or parasite in a sample and for the detection of
CC   at least one antimicrobial agent resistance gene or at least one toxin
CC   gene. hexA nucleic acids are used for the specific and ubiquitous
CC   detection and for identification of Streptococcus pneumoniae. (I) can be
CC   used to design a therapeutic agent which is effective against
CC   microorganisms. Microbial species or genus or family or phylum or group
CC   which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC   Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC   Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
```

CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 870 CCTATCCTGTTTTTGTTAAGCCGGCGC 896

RESULT 14
ADO47257
ID ADO47257 standard; DNA; 1768 BP.
XX
AC ADO47257;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecium vancomycin resistance gene, vanA.
XX
KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanA;
KW gene; ds; hospital acquired infection; VRE;
KW fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecium.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 10; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanA, vancomycin resistance gene.
XX
SQ Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 12; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||||||||||||||||||||||||||
Db 870 CCTATCCTGTTTTTGTTAAGCCGGCGC 896

RESULT 15
ADY59927
ID ADY59927 standard; DNA; 1768 BP.
XX
AC ADY59927;
XX
DT 02-JUN-2005 (first entry)
XX
DE Enterococcus faecium vanA DNA sequence SEQ ID NO:1.
XX
KW DNA detection; antibiotic-resistance; vancomycin; vanA; gene; ds.
XX
OS Enterococcus faecium.
XX
PN US2005058985-A1.
XX
PD 17-MAR-2005.
XX
PF 12-SEP-2003; 2003US-00661094.
XX
PR 12-SEP-2003; 2003US-00661094.
XX
PA (DODG/) DODGSON K J.
XX
PI Dodgson KJ;
XX
DR WPI; 2005-222218/23.
XX
PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX
PS Example 1; SEQ ID NO 1; 33pp; English.
XX
CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecium vanA nucleotide sequence from the present invention.
XX
SQ Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 14; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27

```
                  ||||||||||||||||||||||||||
Db        870 CCTATCCTGTTTTTGTTAAGCCGGCGC 896

RESULT 16
AAT28569
ID   AAT28569 standard; DNA; 2607 BP.
XX
AC   AAT28569;
XX
DT   01-APR-1997  (first entry)
XX
DE   Bacterial antibiotic resitance gene, vanH, vanA and vanX, probe.
XX
KW   Detection; probe; amplification primer; bacterial pathogen; pneumonia;
KW   Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
KW   Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
KW   Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;
KW   Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
KW   Haemophilus influenzae; Moraxella catarrhalis; septicaemia; meningitis;
KW   infection; intra-abdominal infection; skin infection;
KW   bacterial resistance; beta-lactam antibiotic; ds.
XX
OS   Synthetic.
XX
PN   WO9608582-A2.
XX
PD   21-MAR-1996.
XX
PF   12-SEP-1995;   95WO-CA000528.
XX
PR   12-SEP-1994;   94US-00304732.
XX
PA   (BERG/) BERGERON M G.
PA   (OUEL/) OUELLETTE M.
PA   (ROYP/) ROY P H.
XX
PI   Bergeron MG,  Ouellette M,  Roy PH;
XX
DR   WPI; 1996-179953/18.
XX
PT   Method for the detection of bacterial species using probes and primers -
PT   allows detection and quantification of antibiotic resistant bacteria in
PT   patients, the environment and food.
XX
PS   Claim 94; Page 145-147; 216pp; English.
XX
CC   The sequences given in AAT28560-76 represent fragments derived from
CC   bacterial antibiotic resistance genes which were used as probes in the
CC   method of the invention for the detection of bacterial species in a
CC   sample. The method of the invention comprises using probes and/or
CC   amplification primers which are specific, ubiquitous and sensitive for
CC   determining the presence and/or amount of nucleic acids from selected
CC   bacterial species in any sample, where the bacterial nucleic acid
CC   comprises a selected target region hybridisable with the probes or
CC   primers. The method comprises contacting the sample with the probes or
CC   primers and detecting the presence and/or amount of hybridised primers or
CC   amplification products as and indication of the presence and/or amount of
CC   the bacterial species. This method may be used to detect commonly
CC   encountered bacterial pathogens, e.g. Escherichia coli, Klebsiella
CC   pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis, Streptococcus
CC   pneumoniae, Staphylococcus aureus, Staphylococcus epidermidis,
CC   Enterococcus faecalis, Staphylococcus saprophyticus, Streptococcus
CC   pyogenes, Haemophilus influenzae and Moraxella catarrhalis. These
CC   bacterial species are associated with approx. 90% of urinary tract
CC   infections and with a high percentage of other severe infections
CC   including septicaemia, meningitis, pneumonia, intra-abdominal infections,
CC   skin infections and other severe respiratory tract infections. The method
CC   may also be used to evaluate a bacterial resistance to beta- lactam
CC   antibiotics
XX
SQ   Sequence 2607 BP; 768 A; 506 C; 652 G; 681 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 27;  DB 2;  Length 2607;
  Best Local Similarity   100.0%;  Pred. No. 0.035;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db       1455 CCTATCCTGTTTTTGTTAAGCCGGCGC 1481

RESULT 17
ABA76994
ID   ABA76994 standard; DNA; 2607 BP.
XX
AC   ABA76994;
XX
DT   28-JAN-2002  (first entry)
XX
DE   Antibiotic resistance detection polynucleotide SEQ ID NO 170.
XX
KW   Detection; bacterial species; animal; food; environment;
KW   antibiotic resistance; ds.
XX
OS   Unidentified.
XX
PN   NZ501596-A.
XX
PD   29-JUN-2001.
XX
PF   12-SEP-1995;   95NZ-00501596.
XX
PR   12-SEP-1995;   95NZ-00501596.
XX
PA   (IDII-) IDI INFECTIO DIAGNOSTIC INC.
XX
PI   Bergeron MG,  Ouellette M,  Roy PH;
XX
DR   WPI; 2001-615034/71.
XX
PT   Method for detecting target bacterial species in a sample, comprises
PT   detecting the presence or amount of bacterial nucleic acid amplified by a
PT   primer derived from bacterial DNA, specific for the target bacterial
PT   species.
XX
PS   Claim 16; Page 160-162; 168pp; English.
XX
CC   The invention relates to detecting target bacterial species suspected to
CC   be present in a sample, comprising contacting nucleic acids of target
CC   bacterial species with an amplification primer pair derived from a
CC   bacterial DNA fragment (ABA76825-ABA76861) specific for the target
CC   bacterial species but ubiquitous for different strains, amplifying the
CC   nucleic acid and detecting the presence or amount of an amplified
CC   sequence as an indication of the presence or amount of the target
CC   bacterial species. The invention includes primers and probes (ABA76862-
CC   ABA76984) against the target bacterial species, espeially E.coli,
CC   K.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae, S.aureus,
CC   S.epidermidis, E.faecalis, S.saprophyticus, S.pyogenes, H.influenzae,
CC   M.catarrhalis and/or group A Streptococci producing exotoxin A gene spe
CC   A, suspected to be present in a sample which is obtained from human
CC   patients, animals, environment or food, and which consists of one or more
CC   bacterial colonies. Oligonucleotide probes and primers complementary to
CC   the bacterial genes encoding resistance to antibiotics such as bla(tem),
CC   bla(rob), bla(shv), aadB, aacC1, aacC2, aacC3, aacA4, mecA, vanA, vanH,
CC   vanX, satA, aacA-aphD, vat, vga, msrA, sul and/or int (ABA76985-ABA77001)
CC   are also useful to identify commonly encountered and clinically important
CC   resistance genes. The invention provides a rapid method of bacterial
CC   identification that can be achieved, which reduces the time currently
CC   required for the identification of pathogens in the clinical laboratory
XX
SQ   Sequence 2607 BP; 768 A; 506 C; 652 G; 681 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 27;  DB 4;  Length 2607;
  Best Local Similarity   100.0%;  Pred. No. 0.035;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db       1455 CCTATCCTGTTTTTGTTAAGCCGGCGC 1481


RESULT 18
AAH01150
ID   AAH01150 standard; DNA; 3946 BP.
XX
AC   AAH01150;
XX
DT   24-JUL-2001  (first entry)
XX
DE   Enterococcus faecium nucleotide sequence SEQ ID NO:1141.
XX
KW   Species specific; genus specific; family specific; probe; detection;
KW   identification; algal; archaeal; bacterial; fungal; parasitical;
KW   microorganism; diagnosis; translation elongation factor Tu; toxin;
KW   translation elongation factor G; RecA recombinase; resistance;
KW   catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW   primer; ds.
XX
OS   Enterococcus faecium.
XX
PN   WO200123604-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-CA001150.
XX
PR   28-SEP-1999;   99CA-02283458.
PR   19-MAY-2000; 2000CA-02307010.
XX
PA   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI   Bergeron MG,  Boissinot M,  Huletsky A,  Menard C,  Ouellette M;
PI   Picard FJ,  Roy PH;
XX
DR   WPI; 2001-245006/25.
XX
PT   Nucleic acid sequences are used to generate universal probes and primers
PT   which can be used to identify and detect the presence of algal, archaeal,
PT   bacterial, fungal and parasitical species in a test sample.
XX
PS   Disclosure; Page 1035-1036; 1580pp; English.
XX
CC   The present invention describes a method for generating a repertory of
CC   nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC   and/or primers are derived. The method comprises amplifying the nucleic
CC   acids of determined algal, archaeal, bacterial, fungal and parasitical
CC   species with a combination of defined primer pairs. The method can be
CC   used for producing probes and/or primers for detecting one or more
CC   related microorganisms e.g. algae, archaea, bacteria, fungi and
CC   parasites, for universal detection and for specific and ubiquitous
CC   detection and identification of an algal, archaeal, bacterial, fungal and
CC   parasitical species, genus, family and group. A nucleic acid (I) obtained
CC   using the method of the invention can be used for the universal detection
CC   of any bacterium, fungus or parasite in a sample and for the detection of
CC   at least one antimicrobial agent resistance gene or at least one toxin
CC   gene. hexA nucleic acids are used for the specific and ubiquitous
CC   detection and for identification of Streptococcus pneumoniae. (I) can be
CC   used to design a therapeutic agent which is effective against
CC   microorganisms. Microbial species or genus or family or phylum or group
CC   which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC   Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC   Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC   gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC   results than substrate specificity tests as results can be determined in
CC   an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC   represent nucleotide sequences and primers/probes which are given in the
CC   exemplification of the present invention
XX
SQ   Sequence 3946 BP; 1235 A; 706 C; 936 G; 1069 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 27;  DB 4;  Length 3946;
  Best Local Similarity  100.0%;  Pred. No. 0.037;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db       1455 CCTATCCTGTTTTTGTTAAGCCGGCGC 1481


RESULT 19
AAQ25183
ID   AAQ25183 standard; DNA; 7227 BP.
XX
AC   AAQ25183;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   20-NOV-1992  (first entry)
XX
DE   E.faecium antibiotic resistance genes and flanking sequences.
XX
KW   Glycopeptide antibiotic; vancomycin; teicoplanin; resistant;
KW   D-Ala-D-Ala ligase; peptidoglycan precursor; transposon;
KW   inverted repeats; vanR; vanS; vanH; vanA; vanX; ss.
XX
OS   Enterococcus faecium; BM4147.
XX
PN   WO9207942-A1.
XX
PD   14-MAY-1992.
XX
PF   29-OCT-1991;   91WO-FR000855.
XX
PR   31-OCT-1990;   90FR-00013579.
XX
PA   (INSP ) INST PASTEUR.
XX
PI   Arthur M,  Dukta-Malen S,  Molinas C,  Courvalin P;
XX
DR   WPI; 1992-183677/22.
DR   P-PSDB; AAR24305, AAR24306, AAR24307.
XX
PT   Polypeptides involved in expression of glycopeptide antibiotic resistance
PT   - useful in diagnosing presence of Gram-positive enterococcal strains
PT   e.g. Enterococcus Faecium and E Gallinarum.
XX
PS   Disclosure; Fig 4; 163pp; French.
XX
CC   This sequence contains the genes vanH, vanA, vanX, vanR and vanS. The
CC   proteins encoded by the latter two genes (i.e. proteins VanR and VanS)
CC   have a regulatory function and control expression of the other three
CC   ("protective") proteins. See also AAQ25179-Q25182. (Updated on 25-MAR-
CC   2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
CC   (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 7227 BP; 2313 A; 1305 C; 1596 G; 2011 T; 0 U; 2 Other;

  Query Match            100.0%;  Score 27;  DB 2;  Length 7227;
  Best Local Similarity  100.0%;  Pred. No. 0.04;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db       5018 CCTATCCTGTTTTTGTTAAGCCGGCGC 5044


RESULT 20
AAQ25178
ID   AAQ25178 standard; DNA; 10851 BP.
XX
AC   AAQ25178;
```

```
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   20-NOV-1992  (first entry)
XX
DE   E.faecium antibiotic resistance genes and Tn sequences.
XX
KW   Glycopeptide antibiotic; vancomycin; teicoplanin; resistant;
KW   D-Ala-D-Ala ligase; peptidoglycan precursor; transposon;
KW   inverted repeats; ss.
XX
OS   Enterococcus faecium; BM4147.
XX
FH   Key             Location/Qualifiers
FT   CDS             complement(1. .3189)
FT                   /*tag= a
FT                   /product= "transposase"
FT                   /note= "coded by the (-) strand - see AAQ25179"
FT   repeat_unit     1. .38
FT                   /*tag= j
FT                   /rpt_type= INVERTED
FT   CDS             3187. .3762
FT                   /*tag= b
FT                   /product= "resolvase"
FT   CDS             3976. .4671
FT                   /*tag= c
FT                   /product= "VanR"
FT                   /note= "VanR is a transcription activator"
FT   CDS             4649. .5803
FT                   /*tag= d
FT                   /product= "VanS"
FT                   /note= "VanS is a regulatory protein"
FT   CDS             6018. .6986
FT                   /*tag= e
FT                   /product= "VanH"
FT   CDS             6979. .8010
FT                   /*tag= f
FT                   /product= "VanA"
FT   CDS             8016. .8624
FT                   /*tag= g
FT                   /product= "VanX"
FT   CDS             9052. .9963
FT                   /*tag= h
FT                   /product= "VanY"
FT   CDS             10116. .10601
FT                   /*tag= i
FT                   /product= "VanZ"
FT   repeat_unit     complement(10814. .10851)
FT                   /*tag= k
FT                   /rpt_type= INVERTED
XX
PN   WO9207942-A1.
XX
PD   14-MAY-1992.
XX
PF   29-OCT-1991;   91WO-FR000855.
XX
PR   31-OCT-1990;   90FR-00013579.
XX
PA   (INSP ) INST PASTEUR.
XX
PI   Arthur M,  Dukta-Malen S,  Molinas C,  Courvalin P;
XX
DR   WPI; 1992-183677/22.
DR   P-PSDB; AAR24294, AAR24295, AAR24296, AAR24297, AAR24298, AAR24299,
DR   AAR24300, AAR24301, AAR24302.
XX
PT   Polypeptides involved in expression of glycopeptide antibiotic resistance
PT   - useful in diagnosing presence of Gram-positive enterococcal strains
PT   e.g. Enterococcus Faecium and E Gallinarum.
XX
PS   Claim 9; Fig 8; 163pp; French.
XX
CC   This is a transposon sequence. The transposon comprises the genes
CC   necessary for expression of resistance to glycopeptides in Enterococcus
CC   faecium. It also contains genes associated with resistance, e.g. involved
CC   in regulation of expression of the resistance genes or in the amount of
CC   polypeptides produced. See also AAQ25179-Q25183. (Updated on 25-MAR-2003
CC   to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
CC   (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 10851 BP; 3399 A; 1960 C; 2234 G; 3258 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 27;  DB 2;  Length 10851;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db       7472 CCTATCCTGTTTTTGTTAAGCCGGCGC 7498


RESULT 21
AAF76019
ID   AAF76019 standard; DNA; 10851 BP.
XX
AC   AAF76019;
XX
DT   22-MAY-2001  (first entry)
XX
DE   E. faecium VanA vancomycin resistance gene cluster, SEQ ID NO:1.
XX
KW   Vancomycin resistance reduction; antisense expression inhibition;
KW   competitive inducer sequestration; vanH promoter; vanR gene product;
KW   Enterococcus; Staphylococcus; Streptococcus; Gram-positive bacterium;
KW   antibiotic susceptibility; ex vivo eradication; in vivo eradication;
KW   glycopeptide resistance; VanA gene cluster; ds.
XX
OS   Enterococcus faecium.
XX
PN   WO200112803-A2.
XX
PD   22-FEB-2001.
XX
PF   11-AUG-2000; 2000WO-US022086.
XX
PR   17-AUG-1999;   99US-0149313P.
XX
PA   (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI   Inouye RT,  Torres-Viera C,  Moellering R,  Gold H,  Eliopoulos GM;
XX
DR   WPI; 2001-211216/21.
XX
PT   Reducing vancomycin-resistance in vancomycin-resistant organism by
PT   introducing a antisense vancomycin-resistance molecule to inhibit
PT   vancomycin-resistance gene expression, or by enhancing vanH promoter
PT   expression.
XX
PS   Claim 24; Page 41-44; 59pp; English.
XX
CC   The invention relates to methods of reducing vancomycin resistance in a
CC   vancomycin-resistant organism. One method involves introducing a
CC   vancomycin resistance gene antisense nucleic acid into the organism;
CC   antisense oligonucleotides complementary to AAF76023-AAF76031 are
CC   particularly preferred for this purpose. The second method involves
CC   providing additional vanH promoter sequences which are not operatively
CC   coupled to a vancomycin resistance gene, so that the phosphorylated vanR
CC   gene product (which induces vanH promoter activity) is competitively
CC   sequestered. Both methods are able to restore antibiotic susceptibility
CC   in glycopeptide resistant enterococci. The methods of the invention are
CC   useful for reducing vancomycin resistance in a vancomycin resistant
CC   organism, particularly Enterococcus faecium and Enterococcus faecalis,
CC   but also in other Gram-positive bacteria such as Staphylococcus sp. and
CC   Streptococcus sp., to which Enterococcus faecium and Enterococcus
CC   faecalis have the potential to transfer resistance determinants. The
```

```
CC   antisense molecules are useful in the treatment of infection and
CC   colonisation by vancomycin resistant enterococci and other clinically
CC   significant pathogens, and may be used for the ex vivo eradication of
CC   vancomycin-resistant enterococci from frequently colonised settings, such
CC   as intensive care units, haemodialysis units, and chronic care facilities
CC   ; for the in vivo clearance of vancomycin- resistant enterococci from
CC   colonised gastrointestinal or genitourinary tracts of animals, including
CC   humans; and in primary or adjuvant therapy for vancomycin-resistant
CC   enterococcal infections. The gene based strategy targets key vancomycin
CC   resistance determinants and results in restoration of vancomycin
CC   susceptibility in previously glycopeptide- resistant enterococci. The
CC   present sequence represents the Enterococcus faecium VanA gene cluster
XX
SQ   Sequence 10851 BP; 3392 A; 1962 C; 2237 G; 3260 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 27;  DB 4;  Length 10851;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              ||||||||||||||||||||||||||||
Db       7472 CCTATCCTGTTTTTGTTAAGCCGGCGC 7498


RESULT 22
ACA22997
ID   ACA22997 standard; DNA; 1071 BP.
XX
AC   ACA22997;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #4654.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Borrelia burgdorferi.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   P-PSDB; ABU19127.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 14; SEQ ID NO 10867; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1071 BP; 335 A; 127 C; 198 G; 411 T; 0 U; 0 Other;

  Query Match             77.0%;  Score 20.8;  DB 8;  Length 1071;
  Best Local Similarity   91.7%;  Pred. No. 21;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTATCCTGTTTTTGTTAAGCCGGC 25
              |||||||||| |||||||||| ||
Db        498 CTATCCTGTTATTGTTAAGCCCGC 521


RESULT 23
AAX20248_07
Continuation (8 of 10) of AAX20248 from base 700001 (Borrelia burgdorferi polynucleotide
WP Sequence split into 10 fragments  LOCUS AAX20248 Accession Aax20248
WP      Fragment Name       Begin      End
WP      AAX20248_00             1    110000
WP      AAX20248_01        100001    210000
WP      AAX20248_02        200001    310000
WP      AAX20248_03        300001    410000
WP      AAX20248_04        400001    510000
WP      AAX20248_05        500001    610000
WP      AAX20248_06        600001    710000
WP      AAX20248_07        700001    810000
WP      AAX20248_08        800001    910000
WP      AAX20248_09        900001    910715

  Query Match             77.0%;  Score 20.8;  DB 2;  Length 110000;
  Best Local Similarity   91.7%;  Pred. No. 41;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTATCCTGTTTTTGTTAAGCCGGC 25
              |||||||||| |||||||||| ||
Db      10177 CTATCCTGTTRTTGTTAAGCCCGC 10200


RESULT 24
ADO47266/c
ID   ADO47266 standard; DNA; 555 BP.
XX
AC   ADO47266;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Enterococcus vancomycin resistance gene, vanB ENEVANB2A.
XX
KW   Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW   gene; ds; hospital acquired infection; VRE;
KW   fluorescence resonance energy transfer; FRET.
```

XX
OS Enterococcus sp.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 20; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 555 BP; 132 A; 161 C; 115 G; 145 T; 0 U; 2 Other;

Query Match 76.3%; Score 20.6; DB 12; Length 555;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
|||| ||||| ||||| |||||||| |
Db 391 CCTACCCTGTCTTTGTGAAGCCGGCAC 365

RESULT 25
ADO47264/c
ID ADO47264 standard; DNA; 556 BP.
XX
AC ADO47264;
XX
DT 15-JUL-2004 (first entry)
XX
DE Enterococcus vancomycin resistance gene, vanB ENEVANB.
XX
KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW gene; ds; hospital acquired infection; VRE;
KW fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus sp.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 18; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
|||| ||||| ||||| |||||||| |
Db 392 CCTACCCTGTCTTTGTGAAGCCGGCAC 366

RESULT 26
ADO47262/c
ID ADO47262 standard; DNA; 556 BP.
XX
AC ADO47262;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU94526.
XX
KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW gene; ds; hospital acquired infection; VRE;
KW fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOA/) SLOAN L M.
XX

PI Cockerill FR, Sloan LM;
XX
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 15; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 133 A; 162 C; 116 G; 145 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||| ||||| ||||| |||||||| |
Db 392 CCTACCCTGTCTTTGTGAAGCCGGCAC 366

RESULT 27
ADO47263/c
ID ADO47263 standard; DNA; 556 BP.
XX
AC ADO47263;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU94527.
XX
KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW gene; ds; hospital acquired infection; VRE;
KW fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 17; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
||||| ||||| ||||| |||||||| |
Db 392 CCTACCCTGTCTTTGTGAAGCCGGCAC 366

RESULT 28
ADO47261/c
ID ADO47261 standard; DNA; 556 BP.
XX
AC ADO47261;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU94529.
XX
KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW gene; ds; hospital acquired infection; VRE;
KW fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 14; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with

CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
|||| ||||| ||||| |||||||| |
Db 392 CCTACCCTGTCTTTGTGAAGCCGGCAC 366

RESULT 29
ADO47265/c
ID ADO47265 standard; DNA; 556 BP.
XX
AC ADO47265;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU72704.
XX
KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW gene; ds; hospital acquired infection; VRE;
KW fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 19; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 134 A; 158 C; 117 G; 147 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
|||| ||||| ||||| |||||||| |
Db 392 CCTACCCTGTCTTTGTGAAGCCGGCAC 366

RESULT 30
ADO47260/c
ID ADO47260 standard; DNA; 556 BP.
XX
AC ADO47260;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU94528.
XX
KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW gene; ds; hospital acquired infection; VRE;
KW fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 13; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX

```
SQ   Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;

  Query Match            76.3%;  Score 20.6;  DB 12;  Length 556;
  Best Local Similarity  85.2%;  Pred. No. 23;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        392 CCTACCCTGTCTTTGTGAAGCCGGCAC 366


RESULT 31
ADO47259/c
ID   ADO47259 standard; DNA; 556 BP.
XX
AC   ADO47259;
XX
DT   15-JUL-2004  (first entry)
XX
DE   E. faecalis vancomycin resistance gene, vanB EFU94530.
XX
KW   Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KW   gene; ds; hospital acquired infection; VRE;
KW   fluorescence resonance energy transfer; FRET.
XX
OS   Enterococcus faecalis.
XX
PN   US2004058336-A1.
XX
PD   25-MAR-2004.
XX
PF   25-SEP-2002; 2002US-00254260.
XX
PR   25-SEP-2002; 2002US-00254260.
XX
PA   (COCK/) COCKERILL F R.
PA   (SLOA/) SLOAN L M.
XX
PI   Cockerill FR,  Sloan LM;
XX
DR   WPI; 2004-268785/25.
XX
PT   Detecting presence or absence of vancomycin-resistant enterococci in
PT   biological sample from individual comprises using real time polymerase
PT   chain reaction.
XX
PS   Disclosure; SEQ ID NO 16; 23pp; English.
XX
CC   The invention relates to detecting the presence or absence of vancomycin-
CC   resistant enterococci (VRE) in a sample, comprising performing a cycling
CC   step by amplifying a sample with pair of vanA or vanB primers and
CC   hybridising the sample with a pair of vanA or vanB probes, labelled with
CC   donor and acceptor fluorescent group, respectively, detecting
CC   fluorescence resonance energy transfer (FRET), where the presence of FRET
CC   indicates presence of VRE. Also included is an article of manufacture,
CC   comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC   and a donor fluorescent group and a corresponding fluorescent group. The
CC   method is useful for detecting the presence or absence of vancomycin-
CC   resistant enterococci in a biological sample, e.g. stool samples, anal or
CC   perirectal swabs, blood and body fluids from an individual. The method
CC   replaces standard culture methods and reduces the cost. The method
CC   provides rapid vancomycin resistant enterococcus real time PCR assay
CC   which is useful for beginning the antimicrobial therapy immediately to
CC   treat hospital acquired infection. The present sequence is an
CC   enterococcal vanB, vancomycin resistance gene.
XX
SQ   Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;

  Query Match            76.3%;  Score 20.6;  DB 12;  Length 556;
  Best Local Similarity  85.2%;  Pred. No. 23;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        392 CCTACCCTGTCTTTGTGAAGCCGGCAC 366


RESULT 32
AAQ69230
ID   AAQ69230 standard; DNA; 589 BP.
XX
AC   AAQ69230;
XX
DT   25-MAR-2003  (revised)
DT   23-FEB-1995  (first entry)
XX
DE   Enterococcus faecalis vanB gene (internal, amplified fragment).
XX
KW   Gram positive bacteria; inducible glycopeptide resistance; vancomycin;
KW   teicoplanin; antibiotic; vanB gene; ds.
XX
OS   Enterococcus faecalis.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    2. .589
FT                   /*tag=  a
FT                   /note= "amplified internal fragment of vanB gene"
XX
PN   FR2699539-A1.
XX
PD   24-JUN-1994.
XX
PF   18-DEC-1992;   92FR-00015671.
XX
PR   18-DEC-1992;   92FR-00015671.
XX
PA   (INSP ) INST PASTEUR.
XX
PI   Arthur M,  Dutka-Malen S,  Evers S,  Courvalin P;
XX
DR   WPI; 1994-227159/28.
DR   P-PSDB; AAR57150.
XX
PT   New protein VanB involved in bacterial resistance to glyco-peptide(s) -
PT   esp vancomycin, and related nucleic acid, vectors, transformed cells and
PT   antibodies, for in vitro detection of resistant strains.
XX
PS   Claim 8; Page 28; 39pp; French.
XX
CC   The protein encoded by the vanB gene is implicated in resistance of Gram-
CC   positive bacteria to glycopeptides, particularly to vancomycin. This
CC   resistance is inducible by Vancomycin but not by teicoplanin. Sequence
CC   AAQ69230 is a claimed internal fragment of the vanB gene. (Updated on 25-
CC   MAR-2003 to correct PN field.)
XX
SQ   Sequence 589 BP; 163 A; 124 C; 166 G; 136 T; 0 U; 0 Other;

  Query Match            76.3%;  Score 20.6;  DB 2;  Length 589;
  Best Local Similarity  85.2%;  Pred. No. 23;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        165 CCTACCCTGTCTTTGTGAAGCCGGCAC 191


RESULT 33
ADY59941
ID   ADY59941 standard; DNA; 630 BP.
XX
AC   ADY59941;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Enterococcus faecalis vanB DNA sequence SEQ ID NO:15.
XX
```

KW DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS Enterococcus faecalis.
XX
PN US2005058985-A1.
XX
PD 17-MAR-2005.
XX
PF 12-SEP-2003; 2003US-00661094.
XX
PR 12-SEP-2003; 2003US-00661094.
XX
PA (DODG/) DODGSON K J.
XX
PI Dodgson KJ;
XX
DR WPI; 2005-222218/23.
XX
PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX
PS Example 1; SEQ ID NO 15; 33pp; English.
XX
CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecalis vanB nucleotide sequence from the present
CC invention.
XX
SQ Sequence 630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 14; Length 630;
Best Local Similarity 85.2%; Pred. No. 24;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
|||| ||||| ||||| |||||||| |
Db 185 CCTACCCTGTCTTTGTGAAGCCGGCAC 211

RESULT 34
ADY59942
ID ADY59942 standard; DNA; 783 BP.
XX
AC ADY59942;
XX
DT 02-JUN-2005 (first entry)
XX
DE Enterococcus faecalis vanB DNA sequence SEQ ID NO:16.
XX
KW DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS Enterococcus faecalis.
XX
PN US2005058985-A1.
XX
PD 17-MAR-2005.
XX
PF 12-SEP-2003; 2003US-00661094.
XX
PR 12-SEP-2003; 2003US-00661094.
XX
PA (DODG/) DODGSON K J.
XX
PI Dodgson KJ;
XX
DR WPI; 2005-222218/23.
XX
PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX
PS Example 1; SEQ ID NO 16; 33pp; English.
XX
CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecalis vanB nucleotide sequence from the present
CC invention.
XX
SQ Sequence 783 BP; 215 A; 166 C; 223 G; 179 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 14; Length 783;
Best Local Similarity 85.2%; Pred. No. 24;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
|||| ||||| ||||| |||||||| |
Db 392 CCTACCCTGTCTTTGTGAAGCCGGCAC 418

RESULT 35
AAH01126
ID AAH01126 standard; DNA; 801 BP.
XX
AC AAH01126;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecium nucleotide sequence SEQ ID NO:1117.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecium.
XX
PN WO200123604-A2.

XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA001150.
XX
PR 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Disclosure; Page 1027; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 801 BP; 215 A; 169 C; 235 G; 182 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 4; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
|||| ||||| ||||| |||||||| |
Db 389 CCTACCCTGTCTTTGTGAAGCCGGCAC 415

RESULT 36
ADY59937/c
ID ADY59937 standard; DNA; 801 BP.
XX
AC ADY59937;
XX
DT 02-JUN-2005 (first entry)
XX
DE Enterococcus faecium vanB DNA sequence SEQ ID NO:11.
XX
KW DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS Enterococcus faecium.
XX
PN US2005058985-A1.
XX
PD 17-MAR-2005.
XX
PF 12-SEP-2003; 2003US-00661094.
XX
PR 12-SEP-2003; 2003US-00661094.
XX
PA (DODG/) DODGSON K J.
XX
PI Dodgson KJ;
XX
DR WPI; 2005-222218/23.
XX
PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX
PS Example 1; SEQ ID NO 11; 33pp; English.
XX
CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecium vanB nucleotide sequence from the present invention.
XX
SQ Sequence 801 BP; 181 A; 226 C; 169 G; 225 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 14; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
|||| ||||| ||||| |||||||| |
Db 413 CCTACCCTGTCTTTGTGAAGCCGGCAC 387

RESULT 37
ADY59940/c
ID ADY59940 standard; DNA; 801 BP.
XX
AC ADY59940;
XX
DT 02-JUN-2005 (first entry)
XX
DE Enterococcus faecium vanB DNA sequence SEQ ID NO:14.
XX
KW DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS Enterococcus faecium.
XX
PN US2005058985-A1.
XX
PD 17-MAR-2005.
XX
PF 12-SEP-2003; 2003US-00661094.
XX
PR 12-SEP-2003; 2003US-00661094.

```
XX
PA   (DODG/) DODGSON K J.
XX
PI   Dodgson KJ;
XX
DR   WPI; 2005-222218/23.
XX
PT   Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT   e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT   and/or vanB-specific oligonucleotide probes or primers.
XX
PS   Example 1; SEQ ID NO 14; 33pp; English.
XX
CC   The invention relates to a method for detecting vancomycin resistance
CC   gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC   contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC   probe or primer, and detecting or determining the presence or amount of
CC   hybrid formation or amplified nucleic acid. Also described: (1) an
CC   oligonucleotide composition comprising a first oligonucleotide comprising
CC   sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC   898-917 of the vanA gene, or its complement or portion, or an
CC   oligonucleotide comprising sequences substantially corresponding to
CC   nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC   complement or portion, where the oligonucleotide hybridizes under
CC   stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC   comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC   vanB gene in a test sample, comprising the oligonucleotide mentioned
CC   above. The method and kit are useful for detecting and/or amplifying
CC   genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC   antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC   They may also be used in other industrial purposes, such as for quality
CC   control of food, water, pharmaceutical products or other products
CC   requiring microbiological control. The present sequence represents an
CC   Enterococcus faecium vanB nucleotide sequence from the present invention.
XX
SQ   Sequence 801 BP; 183 A; 234 C; 169 G; 215 T; 0 U; 0 Other;

  Query Match             76.3%;  Score 20.6;  DB 14;  Length 801;
  Best Local Similarity   85.2%;  Pred. No. 25;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        413 CCTACCCTGTCTTTGTGAAGCCGGCAC 387


RESULT 38
ADY59943/c
ID   ADY59943 standard; DNA; 801 BP.
XX
AC   ADY59943;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Consensus vanB DNA sequence SEQ ID NO:14.
XX
KW   DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS   Enterococcus faecium.
OS   Enterococcus faecalis.
OS   Synthetic.
XX
PN   US2005058985-A1.
XX
PD   17-MAR-2005.
XX
PF   12-SEP-2003; 2003US-00661094.
XX
PR   12-SEP-2003; 2003US-00661094.
XX
PA   (DODG/) DODGSON K J.
XX
PI   Dodgson KJ;
XX
DR   WPI; 2005-222218/23.
XX
PT   Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT   e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT   and/or vanB-specific oligonucleotide probes or primers.
XX
PS   Example 1; SEQ ID NO 17; 33pp; English.
XX
CC   The invention relates to a method for detecting vancomycin resistance
CC   gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC   contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC   probe or primer, and detecting or determining the presence or amount of
CC   hybrid formation or amplified nucleic acid. Also described: (1) an
CC   oligonucleotide composition comprising a first oligonucleotide comprising
CC   sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC   898-917 of the vanA gene, or its complement or portion, or an
CC   oligonucleotide comprising sequences substantially corresponding to
CC   nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC   complement or portion, where the oligonucleotide hybridizes under
CC   stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC   comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC   vanB gene in a test sample, comprising the oligonucleotide mentioned
CC   above. The method and kit are useful for detecting and/or amplifying
CC   genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC   antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC   They may also be used in other industrial purposes, such as for quality
CC   control of food, water, pharmaceutical products or other products
CC   requiring microbiological control. The present sequence represents a
CC   consensus vanB nucleotide sequence from the present invention.
XX
SQ   Sequence 801 BP; 181 A; 235 C; 169 G; 216 T; 0 U; 0 Other;

  Query Match             76.3%;  Score 20.6;  DB 14;  Length 801;
  Best Local Similarity   85.2%;  Pred. No. 25;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        413 CCTACCCTGTCTTTGTGAAGCCGGCAC 387


RESULT 39
ADY59939/c
ID   ADY59939 standard; DNA; 801 BP.
XX
AC   ADY59939;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Enterococcus faecium vanB DNA sequence SEQ ID NO:13.
XX
KW   DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS   Enterococcus faecium.
XX
PN   US2005058985-A1.
XX
PD   17-MAR-2005.
XX
PF   12-SEP-2003; 2003US-00661094.
XX
PR   12-SEP-2003; 2003US-00661094.
XX
PA   (DODG/) DODGSON K J.
XX
PI   Dodgson KJ;
XX
DR   WPI; 2005-222218/23.
XX
PT   Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT   e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT   and/or vanB-specific oligonucleotide probes or primers.
```

XX
PS Example 1; SEQ ID NO 13; 33pp; English.
XX
CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecium vanB nucleotide sequence from the present invention.
XX
SQ Sequence 801 BP; 183 A; 234 C; 169 G; 215 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 14; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        413 CCTACCCTGTCTTTGTGAAGCCGGCAC 387
```

RESULT 40
ADY59936/c
ID ADY59936 standard; DNA; 801 BP.
XX
AC ADY59936;
XX
DT 02-JUN-2005 (first entry)
XX
DE Enterococcus faecium vanB DNA sequence SEQ ID NO:10.
XX
KW DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS Enterococcus faecium.
XX
PN US2005058985-A1.
XX
PD 17-MAR-2005.
XX
PF 12-SEP-2003; 2003US-00661094.
XX
PR 12-SEP-2003; 2003US-00661094.
XX
PA (DODG/) DODGSON K J.
XX
PI Dodgson KJ;
XX
DR WPI; 2005-222218/23.
XX
PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX
PS Example 1; SEQ ID NO 10; 33pp; English.
XX
CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecium vanB nucleotide sequence from the present invention.
XX
SQ Sequence 801 BP; 182 A; 235 C; 169 G; 215 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 14; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
              |||| ||||| ||||| |||||||| |
Db        413 CCTACCCTGTCTTTGTGAAGCCGGCAC 387
```

Search completed: April 9, 2006, 06:41:33
Job time : 381.134 secs